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80754

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
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jan.delaval@uspto.gov

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	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4445</u>	AA Sequence (#) <input checked="" type="checkbox"/> _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>11/20/02</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>11/21/02</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/> _____
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>112</u>	Other _____	Other (specify) _____

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:21 ; Search time 26.8182 seconds
(without alignments)
879.454 Million cell updates/sec

Title: US-09-787-494-2

Perfect score: 984

Sequence: 1 MTMTDSLAVVLQRRDWNP.....LPGPSDTPLPQTSNNNNH 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq.101002:*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	976	99.2	176	21	AAV57315 Human betahCG/beta
2	894.5	90.9	252	21	AAV57316 Human betahCG/beta
3	795	80.8	209	20	AAV43299 HCG beta subunit-J
4	795	80.8	212	20	AAV43304 HCG beta subunit-J
5	795	80.8	265	22	AAU04602 Single chain gonad
6	795	80.8	265	22	AAU04614 Single chain gonad
7	795	80.8	265	22	AAE04474 Human single chain
8	795	80.8	265	22	AAE04486 Human single chain
9	793	80.6	145	20	AAW93434 Human hCG beta-sub
10	793	80.6	145	20	AAW95520 Human chorionic go

11	793	80.6	145	21	AAB20558 Human chorionic go
12	793	80.6	145	22	AAU04619 Human chorionic go
13	793	80.6	145	22	AAE04491 Human chorionic go
14	793	80.6	145	22	AAU00709 Beta-subunit of hu
15	793	80.6	145	22	AAU01139 Human chorionic go
16	793	80.6	145	22	AAB11765 Beta-human chorion
17	793	80.6	145	22	AAE04121 Beta subunit of hu
18	793	80.6	145	23	AAW50776 Human chorionic go
19	793	80.6	145	23	AAU83014 Beta-human chorion
20	793	80.6	145	12	AAE15043 Human chorionic go
21	793	80.6	145	20	AAU05748 Human chorionic go
22	793	80.6	145	20	AAW99533 Human chorionic go
23	793	80.6	145	21	AAE15358 Human chorionic go
24	793	80.6	145	22	AAE49896 Human chorionic go
25	793	80.6	145	23	AAU96134 Human chorionic go
26	793	80.6	203	20	AAE43298 HCG beta subunit-J
27	793	80.6	206	20	AAE43303 HCG beta subunit-J
28	793	80.6	273	20	AAE43285 HCG beta subunit-J
29	793	80.6	273	20	AAE43292 HCG beta subunit-J
30	791	80.4	212	20	AAE43278 Human CG beta subu
31	790	80.3	165	19	AAW47473 Human beta-hCG pro
32	790	80.3	165	19	AAW33639 Human chorionic go
33	790	80.3	145	19	AAW33637 Human chorionic go
34	789	80.2	145	20	AAW99530 Human chorionic go
35	789	80.2	145	20	AAW99508 Glycoprotein hormo
36	789	80.2	181	22	AAU04613 Gonadotropin analo
37	789	80.2	181	22	AAE04485 Human single chain
38	788.5	80.1	144	12	AAE15178 HCG histidine sub
39	788	80.1	145	12	AAE15171 HCG histidine sub
40	788	80.1	145	12	AAE15173 HCG histidine sub
41	788	80.1	145	20	AAW99514 Glycoprotein hormo
42	788	80.1	145	20	AAW99507 Glycoprotein hormo
43	788	80.0	145	12	AAW99509 Glycoprotein hormo
44	787	80.0	145	20	AAE15169 HCG methionine sub
45	787	80.0	145	14	AAE30999 Human chorionic go

ALIGNMENTS

RESULT 1
AAV57315
ID AAV57315 standard; Protein; 176 AA.
XX
AC AAV57315;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human betahCG/beta-gal fusion protein.
XX
KW Human chorionic gonadotropin; hCG; betahCG; vaccine; chitosan;
KW Infertility; betahCG/beta-gal; fusion protein.
XX
OS Homo sapiens.
XX
PN WO200015253-A1.
XX
PD 23-MAR-2000.
XX
PF 16-SEP-1999; 99WO-US21591.
XX
PR 17-SEP-1998; 98US-0100766.
XX
PA (ZONA-) ZONAGEN INC.
XX
PI Harris J, Martinez M;
XX
DR WPI: 2000-271258/23.
DR N-PSDB: AA290609.
XX
PT Novel human beta-subunit chorionic gonadotropin vaccines used to
PT interrupt fertility in mammals by the immunological inactivation of the
PT pregnancy hormone chorionic gonadotropin

XX Claim 5; Page 32-33; 39pp; English.
 PS The invention provides novel vaccine compositions which comprise the
 CC beta-subunit of human chorionic gonadotropin (betahCG) in combination
 CC with chitosan-based adjuvants. The vaccines are used to induce
 CC infertility especially transient infertility, in female mammals. The
 CC compositions are also used for antibody production. The vaccines comprise
 CC a well-tolerated chitosan-based adjuvant which induces the production of
 CC anti-chorionic gonadotropin antibodies, without inducing the side effects
 CC (e.g. hypersensitivity, erythema, etc.) associated with other adjuvants.
 CC The vaccine also overcomes the problem of non-responsiveness in some
 CC individuals. The present sequence represents a betahCG/beta-gal fusion
 CC protein consisting of leaderless betahCG linked to a beta-gal fragment.
 CC
 XX Sequence 176 AA;
 S0
 Query Match 99.2%; Score 976; DB 21; Length 176;
 Best Local Similarity 100.0%; Pred. No. 2,3e-70;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTMTDSLAVVQLQRDWMENPGCRDLKEPLRPRCRPINATLAVEKGCVCVTNTTICAG 60
 Db 1 MTMTDSLAVVQLQRDWMENPGCRDLKEPLRPRCRPINATLAVEKGCVCVTNTTICAG 60
 QY 61 YCPMTRVLOGLPALPOVVCNRYRDVRFESIRLPGCPRGVNPVSYAVALSCCALCRSS 120
 Db 61 YCPMTRVLOGLPALPOVVCNRYRDVRFESIRLPGCPRGVNPVSYAVALSCCALCRSS 120
 QY 121 TTDCGPRDHPITCDPRFODSSSSKAPPSLPSPSRILPGSPDPIILPOTSHHHHH 176
 Db 121 TTDCGPRDHPITCDPRFODSSSSKAPPSLPSPSRILPGSPDPIILPOTSHHHHH 176
 RESULT 2
 AAY57316
 ID AAY57316 standard; Protein: 252 AA.
 AC AAY57316:
 DT 19-JUN-2000 (first entry)
 XX Alpha-mating factor fragment/betahCG fusion protein.
 DE
 XX Human chorionic gonadotropin; hCG; betahCG; vaccine; chitosan;
 KW Intertility; betahCG/beta-gal; fusion protein.
 OS
 XX Homo sapiens.
 OS
 PN MO200015253-A1.
 XX
 XX 23-MAR-2000.
 PD
 XX 16-SEP-1999; 99WO-US21591.
 PF
 XX 17-SEP-1998; 98US-0100766.
 PR
 XX (ZONA-) ZONAGEN INC.
 PA
 PI Harris J, Martinez M;
 XX
 XX WPI; 2000-271258/23.
 DR N-PSDB; AAZ90610.
 DR
 XX Novel human beta-subunit chorionic gonadotropin vaccines used to
 PT interrupt fertility in mammals by the immunological inactivation of the
 PT pregnancy hormone chorionic gonadotropin -
 XX
 PS Claim 5; Page 34-35; 39pp; English.
 CC The invention provides novel vaccine compositions which comprise the
 CC beta-subunit of human chorionic gonadotropin (betahCG) in combination
 CC with chitosan-based adjuvants. The vaccines are used to induce

CC infertility especially transient infertility, in female mammals. The
 CC compositions are also used for antibody production. The vaccines comprise
 CC a well-tolerated chitosan-based adjuvant which induces the production of
 CC anti-chorionic gonadotropin antibodies, without inducing the side effects
 CC (e.g. hypersensitivity, erythema, etc.) associated with other adjuvants.
 CC The vaccine also overcomes the problem of non-responsiveness in some
 CC individuals. The present sequence represents a betahCG fragment
 CC fused to an alpha-mating factor leader sequence at the N-terminus.
 CC
 XX Sequence 252 AA;
 S0
 Query Match 90.9%; Score 894.5; DB 21; Length 252;
 Best Local Similarity 93.6%; Pred. No. 9.9e-64;
 Matches 162; Conservative 4; Mismatches 2; Indels 5; Gaps 1;
 QY 10 VLQRDWE-----NPGCRDLKEPLRPRCRPINATLAVEKGCVCVTNTTICAGCPT 64
 Db 80 VSLERREAEAVERPDPGCRDLKEPLRPRCRPINATLAVEKGCVCVTNTTICAGCPT 139
 QY 65 MTRVLOGLPALPOVVCNRYRDVRFESIRLPGCPRGVNPVSYAVALSCCALCRSTTDC 124
 Db 140 MTRVLOGLPALPOVVCNRYRDVRFESIRLPGCPRGVNPVSYAVALSCCALCRSTTDC 199
 QY 125 GGRPDHPITCDPRFODSSSSKAPPSLPSPSRILPGSPDPIILPOTSHHHHH 177
 Db 200 GGRPDHPITCDPRFODSSSSKAPPSLPSPSRILPGSPDPIILPOTSHHHHH 252
 RESULT 3
 AAY43299
 ID AAY43299 standard; Protein: 209 AA.
 AC AAY43299:
 DT 19-JAN-2000 (first entry)
 XX HCG beta subunit-Jun fusion protein sequence.
 DE
 XX Cysteine knot protein; protein formation; heterodimeric protein analog;
 KW deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
 KW polycystic ovarian disease; hCG; human; chorionic gonadotropin;
 KW beta subunit; therapy; Jun.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 PN MO9953065-A1.
 XX
 XX 21-OCT-1999.
 PD
 XX 13-APR-1999; 99WO-US08018.
 PF
 XX 14-APR-1998; 98US-0059625.
 PR
 XX (UYNE-) UNIV NEW JERSEY.
 PA
 PI Moyle WR;
 XX
 XX WPI; 1999-620431/53.
 DR
 XX Methods for producing heterodimers, particularly analogues of hormones,
 PT from subunits of cysteine knot proteins -
 PT
 XX Example 7; Fig 20; 73pp; English.
 PS
 CC This sequence is a fusion protein of HCG and Jun. The invention
 CC relates to a method of forming a cysteine knot protein (I) having alpha
 CC and beta-subunits comprising attaching a dimerisation domain (DD) to
 CC either the N-termini of both subunits or the N-terminus of the
 CC alpha-subunit and to the C-terminus of the beta-subunit and dimerising
 CC the products to form a heterodimeric protein analog (II). The method is
 CC used to produce analogues (agonists or antagonists) of deglycosylated
 CC glycoprotein hormones, potentially useful, e.g. for treating infertility

CC where caused by polycystic ovarian disease (associated with excessive
 CC levels of luteinising hormone). Products that retain DD's are also useful
 CC as immunogens or antigens (since a PD may contain highly antigenic
 CC amino acid sequences). Attachment of a DD (which may be removed later)
 CC facilitates the formation of heterodimers, that have similar structures
 CC (and thus receptor-binding and immunogenic properties) to native dimers,
 CC and allows the combination of subunits that would otherwise combine
 CC poorly, or not at all. The N-terminal part of a glycoprotein hormone may
 CC be modified without loss of activity, and attachment of the DD reduces
 CC formation of homodimers. Heterodimers have longer circulation times in
 CC vivo than individual subunits.

XX Sequence 209 AA:

Query Match 80.8%; Score 795; DB 20; Length 209;
 Best Local Similarity 99.3%; Pred. No. 6.9e-56;
 Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 26 KEPLRPRCPINATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVNCYRD 85
 DB 22 KEPLRPRCPINATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVNCYRD 81
 OY 86 VRFESIRLPGCGRVNPNVSYAVALSQCACLCRRSTTDCGPRDHLPTCDPRFODSSSS 145
 DB 82 VRFESIRLPGCGRVNPNVSYAVALSQCACLCRRSTTDCGPRDHLPTCDPRFODSSSS 141
 OY 146 KAPPSLPSPSRLLPGSPDPTLPQTS 171
 DB 142 KAPPSLPSPSRLLPGSPDPTLPQTS 167

RESULT 4
 ID AAY43304
 AAY43304 standard; Protein; 212 AA.

XX AC AAY43304;

XX DT 19-JAN-2000 (first entry)

XX DE HCG beta subunit-Jun fusion protein sequence.

KW Cysteine knot protein; protein formation; heterodimeric protein analog;
 KW deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
 KW polycystic ovarian disease; hcg; human; chorionic gonadotropin;
 KW beta subunit; therapy; Jun.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN W09953065-A1.

XX PD 21-OCT-1999.

XX PF 13-APR-1999; 99WO-US08018.

XX PR 14-APR-1998; 98US-0059625.

XX PA (UYNE-) UNIV NEW JERSEY.

XX PI Moyle WR;

XX DR WPI; 1999-620431/53.

XX PT Methods for producing heterodimers, particularly analogues of hormones,
 PT from subunits of cysteine knot proteins -

XX Example 7; Fig 20; 73pp; English.

CC This sequence is a fusion protein of HCG and Jun. The invention
 CC relates to a method of forming a cysteine knot protein (1) having alpha
 CC and beta subunits comprising attaching a dimerisation domain (DD) to
 CC either the N-termini of both subunits or the N-terminus of the
 CC alpha-subunit and to the C-terminus of the beta-subunit and dimerising

CC the products to form a heterodimeric protein analog (II). The method is
 CC used to produce analogues (agonists or antagonists) of deglycosylated
 CC glycoprotein hormones, potentially useful, e.g. for treating infertility
 CC where caused by polycystic ovarian disease (associated with excessive
 CC levels of luteinising hormone). Products that retain DD's are also useful
 CC as immunogens or antigens (since a PD may contain highly antigenic
 CC amino acid sequences). Attachment of a DD (which may be removed later)
 CC facilitates the formation of heterodimers, that have similar structures
 CC (and thus receptor-binding and immunogenic properties) to native dimers,
 CC and allows the combination of subunits that would otherwise combine
 CC poorly, or not at all. The N-terminal part of a glycoprotein hormone may
 CC be modified without loss of activity, and attachment of the DD reduces
 CC formation of homodimers. Heterodimers have longer circulation times in
 CC vivo than individual subunits.

XX Sequence 212 AA:

Query Match 80.8%; Score 795; DB 20; Length 212;
 Best Local Similarity 99.3%; Pred. No. 7e-56;
 Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 26 KEPLRPRCPINATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVNCYRD 85
 DB 22 KEPLRPRCPINATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVNCYRD 81
 OY 86 VRFESIRLPGCGRVNPNVSYAVALSQCACLCRRSTTDCGPRDHLPTCDPRFODSSSS 145
 DB 82 VRFESIRLPGCGRVNPNVSYAVALSQCACLCRRSTTDCGPRDHLPTCDPRFODSSSS 141
 OY 146 KAPPSLPSPSRLLPGSPDPTLPQTS 171
 DB 142 KAPPSLPSPSRLLPGSPDPTLPQTS 167

RESULT 5
 ID AAU04602
 AAU04602 standard; Protein; 265 AA.

XX AC AAU04602;

XX DT 23-OCT-2001 (first entry)

XX DE Single chain gonadotropin analogue #1.

XX KW Human; glycoprotein hormone; infertility; in vivo fertilisation;
 KW single chain gonadotropin.

XX OS Homo sapiens.

XX PN US6242580-B1.

XX PD 05-JUN-2001.

XX PF 31-MAR-1999; 99US-0282357.

XX PR 25-AUG-1997; 97US-0918288.

XX PR 18-FEB-1994; 94US-0199382.

XX PR 12-AUG-1994; 94US-0289396.

XX PR 22-SEP-1994; 94US-0310590.

XX PR 04-NOV-1994; 94US-0334628.

XX PR 07-DEC-1994; 94US-0351591.

XX PR 07-JUN-1995; 95US-0475049.

XX PR 09-MAY-1997; 97US-0853524.

XX PA (UNITV) UNIV WASHINGTON.

XX PI Boime I, Moyle WR;
 XX DR WPI; 2001-424301/45.
 XX DR N-PSDB; AAS08485.
 XX PT New single chain forms of the glycoprotein hormone quartet useful for
 PT generating antibodies specifically immunoreactive with the new

PT compounds, in treating infertility, or as aids for in vivo
PT fertilization techniques -
XX
XX Example 5; Fig 5; 86pp; English.

XX The sequence represents the amino acid sequence of single chain
CC gonadotropin analogue #1. The glycoprotein hormone analogue is
CC useful for generating antibodies specifically immunoreactive with new
CC compounds, as a substitute for the heterodimeric forms of the hormones,
CC in the treatment of infertility, as an aid for in vivo fertilisation
CC techniques, and in other therapeutic methods associated with the native
CC hormone. The single chain protein is further useful as a reagent in a
CC manner similar to the heterodimer, as a diagnostic tool to detect the
CC presence of antibodies with respect to the native proteins in the
CC biological samples, as a control reagent in assay kits for assessing the
CC levels of these hormones in various samples, and in detecting and
CC purifying receptors to which the native hormones bind. The single chain
CC forms of the heterodimers or homodimers have the following advantages
CC production are reduced since only a single gene is needed to recombinant
CC translate and process, provide an alternate form thus permitting fine
CC tuning of activity levels and of in vivo half lives. Single chain forms
CC are unique starting materials for identifying truncated forms with the
CC activity of the dimer. The linkage between the subunits permits the
CC protein to be engineered without disturbing the overall folding of the
CC protein.

XX Sequence 265 AA:

Query Match 80.8%; Score 795; DB 22: Length 265;
Best Local Similarity 99.3%; Pred. No. 8.7e-56;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 KEPLRRCRPNATLAVKEGCPVCITYNTTICAGYCPMTMRVLQGVLPALPQVVCNWRD 85
DB 22 KEPLRRCRPNATLAVKEGCPVCITYNTTICAGYCPMTMRVLQGVLPALPQVVCNWRD 81
QY 86 VFESIRLPGCGRGVNPVSYAVALSCCALCRSTTDCGPKRHPRLTCDPRFODSSSS 145
DB 82 VFESIRLPGCGRGVNPVSYAVALSCCALCRSTTDCGPKRHPRLTCDPRFODSSSS 141
QY 146 KAPPSLPSPSRRLPGPSDTPILPGS 171
DB 142 KAPPSLPSPSRRLPGPSDTPILPGS 167

RESULT 6
AAU04614
ID AAU04614 standard; Protein; 265 AA.
XX

AC AAU04614;

DT 23-OCT-2001 (first entry)

DE Single chain gonadotropin analogue #1a.

KW Human; glycoprotein hormone; Infertility; in vivo fertilisation;
XX single chain gonadotropin.

OS Homo sapiens.

PN US6242580-B1.

PD 05-JUN-2001.

PF 31-MAR-1999; 99US-0282357.

PR 25-AUG-1997; 97US-0918288.

PR 18-FEB-1994; 94US-0193382.

PR 12-AUG-1984; 94US-0289396.

PR 22-SEP-1994; 94US-0310590.

PR 04-NOV-1994; 94US-0334628.

PR 07-DEM-1994; 94US-0351591.

PR 07-JUN-1995; 95US-0475049.
PR 09-MAY-1997; 97US-0855524.
XX
XX (UNITW) UNITW WASHINGTON.

PA Bolme I, Moyle WR;

PI WPI; 2001-424301/45.

DR N-PSDB; AAS08509.

PT New single chain forms of the glycoprotein hormone quartet useful for
PT generating antibodies specifically immunoreactive with the new
PT compounds. In treating infertility, or as aids for in vivo
PT fertilization techniques -

XX Example 16; Fig 17; 86pp; English.

XX The sequence represents the amino acid sequence of single chain
CC gonadotropin analogue #1a. The glycoprotein hormone analogue is
CC useful for generating antibodies specifically immunoreactive with new
CC compounds, as a substitute for the heterodimeric forms of the hormones,
CC in the treatment of infertility, as an aid for in vivo fertilisation
CC techniques, and in other therapeutic methods associated with the native
CC hormone. The single chain protein is further useful as a reagent in a
CC manner similar to the heterodimer, as a diagnostic tool to detect the
CC presence of antibodies with respect to the native proteins in the
CC biological samples, as a control reagent in assay kits for assessing the
CC levels of these hormones in various samples, and in detecting and
CC purifying receptors to which the native hormones bind. The single chain
CC forms of the heterodimers or homodimers have the following advantages
CC production are reduced since only a single gene is needed to recombinant
CC translate and process, provide an alternate form thus permitting fine
CC tuning of activity levels and of in vivo half lives. Single chain forms
CC are unique starting materials for identifying truncated forms with the
CC activity of the dimer. The linkage between the subunits permits the
CC protein to be engineered without disturbing the overall folding of the
CC protein.

XX Sequence 265 AA:

Query Match 80.8%; Score 795; DB 22: Length 265;
Best Local Similarity 99.3%; Pred. No. 8.7e-56;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 KEPLRRCRPNATLAVKEGCPVCITYNTTICAGYCPMTMRVLQGVLPALPQVVCNWRD 85
DB 22 KEPLRRCRPNATLAVKEGCPVCITYNTTICAGYCPMTMRVLQGVLPALPQVVCNWRD 81
QY 86 VFESIRLPGCGRGVNPVSYAVALSCCALCRSTTDCGPKRHPRLTCDPRFODSSSS 145
DB 82 VFESIRLPGCGRGVNPVSYAVALSCCALCRSTTDCGPKRHPRLTCDPRFODSSSS 141
QY 146 KAPPSLPSPSRRLPGPSDTPILPGS 171
DB 142 KAPPSLPSPSRRLPGPSDTPILPGS 167

RESULT 7
AAE04474
ID AAE04474 standard; Protein; 265 AA.
XX

AC AAE04474;

DT 04-SEP-2001 (first entry)

DE Human single chain gonadotropin analog no:1.

KW Human; single chain gonadotropin analog no:1; anti-infertility; drug;
KW peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
KW FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
KW glycoprotein; infertility; fusion protein.

XX

OS	Homo sapiens.
XX	Synthetic.
FH	Key
FT	Region
FT	Location/Qualifiers 21..165
FT	/note= "Corresponds to 1-145 amino acids of human chorionic gonadotropin (CG) beta-subunit"
FT	Region
FT	/note= "Linker peptide" 174..265
FT	/note= "Corresponds to 1-92 amino acids of human single chain gonadotropin alpha-subunit"
FX	
PX	US6238890-B1.
PN	
PD	29-MAY-2001.
PF	25-AUG-1997; 97US-0918288.
PX	
PR	18-FEB-1994; 94US-0199382. 12-AUG-1994; 94US-0289396. 22-SEP-1994; 94US-0310599. 04-NOV-1994; 94US-0334628. 07-DEC-1994; 94US-0351591. 07-JUN-1995; 95US-0475049. 09-MAY-1997; 97US-0853524.
PA	(UNIM) UNIV WASHINGTON.
PI	
PL	Boime I, Moyle WR;
DR	WPI: 2001-366474/38.
DR	N-PSDB; AAD08785.
PX	
PT	New DNA or RNA encoding single chain protein useful in treating infertility, as aids in vitro fertilization techniques, or other therapeutic methods associated with the native hormones -
PX	
PS	Claim 9; Fig 5; 87pp: English.
CC	The invention relates to human single chain forms of the glycoprotein hormone quartet which is an agonist or antagonist of luteinising hormone (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers having identical alpha subunits and differing beta subunits. The agonist forms of single chain hormones are used in treating infertility, as aids in vitro fertilisation techniques, and other therapeutic methods associated with the native hormones. The single chain hormones are useful as reagents in a manner similar to heterodimers, as diagnostic tools to detect the presence of antibodies with respect to the native proteins in biological samples, as control reagents in assay kits for assessing the levels of these hormones in various samples, in detecting and purifying receptors to which the native hormones bind. The single chain hormones are also used in affinity chromatographic preparation of receptors or antihormone antibodies. They are used as purification tools for isolation of subsequent preparations of these materials and to monitor levels of single chain hormones administered as drugs. The single chain glycoproteins are used to generate antibodies specifically immunoreactive with these new compounds, as substitutes for the heterodimeric forms of hormones. The present sequence is human single chain gonadotropin analog no:1 related to the invention. Analog no:1 is a fusion protein consisting of human chorionic gonadotropin (CG) beta-subunit (1-145 amino acids) fused to human single chain gonadotropin alpha-subunit (1-92 amino acids) by a linker sequence. This analog serves as a useful starting compound for template directed vaccine design and for the development of hormone-specific vaccines for use in humans.
Sequence	265 AA:
Query Match	80.8%; Score 795; DB 22; Length 265;
Best Local Similarity	99.3%; Pred. No. 8.7e-56;
Matches 145; Conservative	0; Mismatches 1; Indels 0; Gaps 0;

Oy	26	KEPLRRCRPIINATLAVEKEGCPVCIYVNTTTCAGICPTMRVLOGVLPALPQVYCNRRD	85
Db	22	KEPLRRCRPIINATLAVEKEGCPVCIYVNTTTCAGICPTMRVLOGVLPALPQVYCNRRD	81
Oy	86	VRFESIRLPGCGRGVNPVYSVAVALSCCAlCRSTTCCGGRKHDPHLCDDPRFDSSSS	145
Db	82	VRFESIRLPGCGRGVNPVYSVAVALSCCAlCRSTTCCGGRKHDPHLCDDPRFDSSSS	141
Oy	146	KAPPSLPSPSRLPGPSDTPILPQTS	171
Db	142	KAPPSLPSPSRLPGPSDTPILPQTS	167
RESULT 8			
AE04486	AAE04486 standard; Protein: 265 AA.		
AC	AAE04486;		
XX	04-SEP-2001 (first entry)		
XX	Human single chain gonadotropin analog no:1a.		
XX	Human; single chain gonadotropin analog no:1a; anti-infertility; drug;		
KW	peptide therapy; luteinising hormone; LH; follicle stimulating hormone;		
KW	FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;		
KW	glycoprotein; infertility; fusion protein; mutant; mutein.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	21..165	
FT		/note="Corresponds to 1-145 amino acids of human	
FT	Region	166..173	
FT		/note="Linker peptide"	
FT	Region	174..265	
FT		/note="Corresponds to 1-92 amino acids of human single	
FT		chain gonadotropin alpha-subunit"	
FT	Misc-difference	225	
FT		/note="Wild type Asn substituted with Gln"	
FT	Misc-difference	251	
FT		/note="Wild type Asn substituted with Gln"	
XX			
PN	US6238890-B1.		
XX			
PD	29-MAY-2001.		
XX			
PE	25-AUG-1997;	97US-0918288.	
XX			
PR	18-FEB-1994;	94US-0199382.	
PR	12-AUG-1994;	94US-0289396.	
PR	22-SEP-1994;	94US-0310590.	
PR	04-NOV-1994;	94US-0334628.	
PR	07-DEC-1994;	94US-0351591.	
PR	07-JUN-1995;	95US-0475049.	
PR	09-MAY-1997;	97US-0853524.	
XX			
PA	(UNIV) UNIV WASHINGTON.		
XX			
PI	Boime I, Moyle WR;		
XX			
DR	WPI: 2001-366474/38.		
XX			
DR	N-PSDB; AAD08809.		
XX			
PT	New DNA or RNA encoding single chain protein useful in treating		
PT	infertility, as aids in vitro fertilization techniques, or other		
PT	therapeutic methods associated with the native hormones		
XX			
SS	Claim 9; Fig 17; 87pp; English.		
XX			
CC	The invention relates to human single chain forms of the glycoprotein		

CC hormone quartet which is an agonist or antagonist of luteinising hormone
 CC (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
 CC (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
 CC having identical alpha subunits and differing beta subunits. The agonist
 CC forms of single chain hormones are used in treating infertility, as aids
 CC in vitro fertilisation techniques, and other therapeutic methods
 CC associated with the native hormones. The single chain hormones are useful
 CC as reagents in a manner similar to heterodimers, as diagnostic tools to
 CC detect the presence of antibodies with respect to the native proteins in
 CC biological samples, as control reagents in assay kits for assessing the
 CC levels of these hormones in various samples, in detecting and purifying
 CC receptors to which the native hormones bind. The single chain hormones
 CC are also used in affinity chromatographic preparation of receptors or
 CC antihormone antibodies. They are used as purification tools for
 CC isolation of subsequent preparations of these materials and to monitor
 CC levels of single chain hormones administered as drugs. The single chain
 CC glycoproteins are used to generate antibodies specifically immunoreactive
 CC with these new compounds, as substitutes for the heterodimeric forms of
 CC hormones. The present sequence is human single chain gonadotropin analog
 CC no:1a related to the invention. Analog no:1a is a fusion protein
 CC consisting of human chorionic gonadotropin (CG) beta-subunit (1-145 amino
 CC acids) fused to human single chain gonadotropin alpha-subunit (1-92 amino
 CC acids) by a linker sequence. This analog serves as a useful starting
 CC compound for template directed vaccine design and for the development of
 CC hormone-specific vaccines for use in humans.

XX Sequence 265 AA:

Query Match 80.8%; Score 795; DB 22; Length 265;
 Best Local Similarity 99.3%; Pred. No. 8.7e-56;
 Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVVCNRYD 85
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 22 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVVCNRYD 81
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 86 VFESIRLPGCRGVNPNVSVAVALSCCALCRSTTDCGGRKDHPLTCDPRFQDSSSS 145
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 82 VFESIRLPGCRGVNPNVSVAVALSCCALCRSTTDCGGRKDHPLTCDPRFQDSSSS 141
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 146 KAPPSLPSPSRRLPGSDPTPLPQ 171
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 142 KAPPSLPSPSRRLPGSDPTPLPQGS 167
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9
 AAW93434 standard; peptide: 145 AA.

XX AAW93434;
 AC 11-JUN-1999 (first entry)
 XX
 DT Human hCG beta-subunit peptide structure I.
 XX
 DE Human chorionic gonadotropin; beta subunit; antigenic peptide; hCG;
 KW contraceptive; vaccine; fertility; polyclonal antisera; diagnostic;
 KW immunogen; human luteinising hormone.
 XX
 OS Homo sapiens.
 XX
 PN US5891992-A.
 PD 06-APR-1999.
 XX
 PD 06-JUN-1995; 95US-0467569.
 PF
 XX 07-AUG-1989; 89US-0390530.
 PR 04-DEC-1985; 85US-0804642.
 PR 17-AUG-1987; 87US-0086401.
 PR 06-OCT-1992; 92US-0958601.
 PR 06-JUN-1995; 95US-0467569.
 PF
 XX

PA (OHIS) UNIV OHIO STATE RES FOUND.

PI Stevens VC:

XX WPI; 1999-253928/21.

PT Synthetic antigenic peptides from human chorionic gonadotropin
 PT beta-subunit

PS Disclosure: Column 19; 80pp; English.

CC This invention describes novel synthetic antigenic peptides (A) based
 CC on the human chorionic gonadotropin (hCG) beta-subunit. These peptides
 CC have contraceptive properties and are used for the development of
 CC vaccines used to control fertility in animals and to generate
 CC polyclonal antisera for diagnostic use. The peptides are more specific
 CC immunogens than corresponding unmodified peptides from hCG beta-subunit,
 CC i.e. they do not elicit antibodies that cross-react with human
 CC luteinising hormone.

XX Sequence 145 AA:

Query Match 80.6%; Score 793; DB 20; Length 145;
 Best Local Similarity 100.0%; Pred. No. 7e-56;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVVCNRYD 85
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 2 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVVCNRYD 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 86 VFESIRLPGCRGVNPNVSVAVALSCCALCRSTTDCGGRKDHPLTCDPRFQDSSSS 145
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 62 VFESIRLPGCRGVNPNVSVAVALSCCALCRSTTDCGGRKDHPLTCDPRFQDSSSS 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 146 KAPPSLPSPSRRLPGSDPTPLPQ 169
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 122 KAPPSLPSPSRRLPGSDPTPLPQ 145
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
 AAW95520 standard; protein: 145 AA.

XX AAW95520;

XX 24-MAR-1999 (first entry)

XX Human chorionic gonadotropin (hCG) beta subunit.

XX Human; chorionic gonadotropin; hCG; three-dimensional; 3D; analogue;
 KW molecular simulation; visual display; chemical structure; growth factor;
 KW N-glycosylation site; follicle stimulating hormone; luteinising hormone;
 KW thyroid stimulating hormone; in vitro fertilisation; fertility; mutation;
 KW beta subunit; glycoprotein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 64 /note- "wild-type phe at this position can be mutated
 FT to Asn to introduce a new N-glycosylation site;
 FT see claim 3"

FT Misc-difference 79 /note- "wild-type Val at this position can be mutated
 FT to Asn to introduce a new N-glycosylation site;
 FT see claim 3"

XX US5864488-A.

XX 26-JAN-1999.

XX 24-FEB-1995; 95US-0395238.

PR 24-FEB-1994; 94GB-0003600.
XX
XX (UNIU) UNIV GLASGOW.
PA
PI Grooteenhuis PDJ, Harris DC, Isaacs NW, Laphorn AJ;
XX WPI; 1999-131522/11.
XX
XX
XX Determining the 3-dimensional coordinates of chorionic gonadotropin
PT and computer-assisted re-design of the chemical structure - used for
PT production of gonadotropin hormone analogues
XX
XX Examples; Fig 2; 60pp; English.
XX
XX The invention relates to determining whether an analogue of human
CC chorionic gonadotropin (hCG) will have an altered three-dimensional (3D)
CC structure as compared to hCG. Analogues of hCG and other glycoprotein
CC hormones are produced by inputting chemical changes to the 3D structure
CC into a computer loaded with 3D molecular simulation software and
CC representing visually on a computer display. On inputting into the data
CC input of the computer at least one operator change in chemical structure
CC of the hCG molecule, the molecular simulation software produces a
CC modified 3D molecular representation of the analogue structure. The 3D
CC representation of the analogue can be displayed on the visual display,
CC whereby changes in 3D structure of the hCG molecule consequent on changes
CC in chemical structure can be visually determined. Glycoprotein analogues
CC with additional glycosylation sites, and analogues with non-essential
CC hairpins deleted can be produced by this method. The methods can be used
CC to obtain analogues of hCG, follicle stimulating hormone, luteinising
CC hormone, thyroid stimulating hormone, which may act as agonists or
CC antagonists. The analogues can be used as growth factors in mammals, for
CC in vitro fertilisation techniques and for treatment in vivo to enhance
CC fertility. The present sequence represents the beta subunit of hCG.
CC N-glycosylation sites can be introduced by single point mutations at
CC specified positions to produce hCG analogues.
XX
XX Sequence 145 AA:
SQ
Query Match 80.6%; Score 793; DB 20; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 KEPLRRCRPIINATLAVEKEGCPVCITVNTTICAGCPTMTFVLOGVLPALPQVVCNRYD 85
DB 2 KEPLRRCRPIINATLAVEKEGCPVCITVNTTICAGCPTMTFVLOGVLPALPQVVCNRYD 61
QY 86 VFRESIRLPGCGRGVNPVSYAVALSQCQALCRSTTDCGGRKDHPLTCDPRFQDSSSS 145
DB 62 VFRESIRLPGCGRGVNPVSYAVALSQCQALCRSTTDCGGRKDHPLTCDPRFQDSSSS 121
QY 146 KAPPSLPSPRLPGSPDPILPQ 169
DB 122 KAPPSLPSPRLPGSPDPILPQ 145
RESULT 11
ID AAB20558 standard; protein; 145 AA.
XX
XX AAB20558;
XX
XX 11-DEC-2000 (first entry)
XX
XX Human chorionic gonadotropin beta subunit amino acid sequence.
XX
XX Human; Chorionic gonadotropin antigen; follicle stimulating hormone;
KW contraception; abortion; hormone related disease; carcinoma; cytostatic;
KW contraceptive; antifertility; antihypertensive; antidiabetic; vaccine;
KW fertility; cancer; hypertension; diabetes.
XX
XX Homo sapiens.
XX
XX US6096318-A.

XX
XX 01-AUG-2000.
PD
XX
XX 06-JUN-1995; 95US-0466445.
PF
XX
XX 25-AUG-1978; 78US-0936876.
PR 15-JUL-1987; 87US-0073748.
PR 26-AUG-1992; 92US-0935331.
PR 17-FEB-1989; 89US-0311331.
PR 07-MAY-1973; 73US-0357892.
PR 16-OCT-1973; 73US-0406821.
PR 22-APR-1974; 74US-0462855.
PR 14-OCT-1975; 75US-0622031.
PR 16-JAN-1980; 80US-0112628.
PR 20-NOV-1981; 81US-0323690.
PR 18-MAY-1983; 83MO-US00777.
PR 02-NOV-1984; 84US-0667863.
XX
XX (OHIS) UNIV OHIO STATE.
XX
XX Stevens VC;
XX
XX WPI; 2000-542298/49.
XX
XX
XX New antigen for treating hormone related diseases, is conjugated with a
PT specific polypeptide which elicits an antibody response against human
PT chorionic gonadotropin -
XX
XX
XX Disclosure; Column 18; 61pp; English.
XX
XX The present invention describes an antigen (A) comprising a carrier
CC chemically conjugated with a polypeptide (I) capable of eliciting
CC antibody response to human chorionic gonadotropin (CG) and not to human
CC luteinising hormone (LH), or a polypeptide (II) capable of eliciting
CC antibody response to human CG. (A) has cytostatic, contraceptive,
CC antifertility, antihypertensive and antidiabetic activities, and can
CC be used as part of a vaccine. (A) is useful for contraception, abortion
CC and for treating hormone related diseases, for treating hormone
CC associated carcinomas and to boost an animals' resistance to exogenous
CC proteins e.g. viral proteins. (A) is also useful in animal fertility
CC control, for treating cancer, hypertension, diabetes and related vascular
CC diseases. (A), safely and effectively controls various disease states
CC or maladies caused or influenced by unusual excesses of certain
CC polypeptides such as gastrin, angiotensin II or somatomedin. It also
CC provides an effective and safe method of terminating a pregnancy soon
CC after conception which does not have serious harmful side effects.
CC The present sequence represents the human CG beta subunit amino acid
CC sequence, which is given in the exemplification of the present
XX invention.
XX
XX Sequence 145 AA:
SQ
Query Match 80.6%; Score 793; DB 21; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 KEPLRRCRPIINATLAVEKEGCPVCITVNTTICAGCPTMTFVLOGVLPALPQVVCNRYD 85
DB 2 KEPLRRCRPIINATLAVEKEGCPVCITVNTTICAGCPTMTFVLOGVLPALPQVVCNRYD 61
QY 86 VFRESIRLPGCGRGVNPVSYAVALSQCQALCRSTTDCGGRKDHPLTCDPRFQDSSSS 145
DB 62 VFRESIRLPGCGRGVNPVSYAVALSQCQALCRSTTDCGGRKDHPLTCDPRFQDSSSS 121
QY 146 KAPPSLPSPRLPGSPDPILPQ 169
DB 122 KAPPSLPSPRLPGSPDPILPQ 145
RESULT 12
ID AAU04619 standard; protein; 145 AA.
XX
XX AAU04619

```

AC  AAU04619;
XX
DT  23-OCT-2001 (first entry)
XX
DE  Human chorionic gonadotropin (hCG) beta, amino acids 1-145.
XX
KM  Human; chorionic gonadotropin; hCG; glycoprotein hormone; infertility;
KW  luteinising hormone; LH; follicle stimulating hormone; FSH;
XX  thyroid stimulating hormone; TH.
XX
OS  Homo sapiens.
XX
PN  US6242580-B1.
XX
PD  05-JUN-2001.
XX
PF  31-MAR-1999; 99US-0282357.
XX
PR  25-AUG-1997; 97US-0918288.
XX  18-FEB-1994; 94US-0199382.
XX  12-AUG-1994; 94US-0289396.
XX  22-SEP-1994; 94US-0310590.
XX  04-NOV-1994; 94US-0334628.
XX  07-DEC-1994; 94US-0351591.
XX  07-JUN-1995; 95US-0475049.
XX  09-MAY-1997; 97US-0853524.
XX
PA  (UNITW ) UNITW WASHINGTON.
XX
PI  Bolme I, Moyle WR;
XX
DR  WPI; 2001-424301/45.
XX
PT  New single chain forms of the glycoprotein hormone quartet useful for
PT  generating antibodies specifically immunoreactive with the new
PT  compounds in treating infertility, or as aids for in vivo
PT  fertilization techniques.
XX
PS  Example 19; Column 34; 86pp; English.
XX
XX  The sequence represents the amino acid sequence of human chorionic
XX  gonadotropin (hCG) beta, amino acids 1-145. The protein is an
XX  important glycoprotein hormone heterodimer, along with luteinising
XX  hormone (LH), follicle stimulating hormone (FSH), thyroid stimulating
XX  hormone (TH), which all have identical alpha subunits but differing beta
XX  subunits. The proteins are useful for generating antibodies specifically
XX  immunoreactive with new compounds, as substitutes for the
XX  heterodimeric forms of the hormones, in the treatment of infertility, as
XX  aids for in vivo fertilisation techniques, and in other therapeutic
XX  methods associated with the native hormones. The single chain proteins
XX  are further useful as reagents in a manner similar to the heterodimers,
XX  as diagnostic tools to detect the presence of antibodies with respect to
XX  the native proteins in the biological samples, as control reagents in
XX  assay kits for assessing the levels of these hormones in various samples,
XX  and in detecting and purifying receptors to which the native hormones
XX  bind. The single chain forms of the heterodimers or homodimers have the
XX  following advantages over their dimeric forms: they are more stable,
XX  problems of recombinant production are reduced since only a single gene
XX  is needed to transcribe, translate and process, provide an alternate form
XX  thus permitting fine tuning of activity levels and of in vivo half lives.
XX  Single chain forms are unique starting materials for identifying
XX  truncated forms with the activity of the dimer. The linkage between the
XX  subunits permits the protein to be engineered without disturbing the
XX  overall folding of the protein.
XX
SQ  Sequence 145 AA;

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DB  2 KEPLRRCPRIATLAVEKEGCPVCITVNTTICAGYCPTMTRVLOGVLPALPOVVCNRYD 61
QY  86 VRFESIRLPGCPGVNPPVSVAVLSCCALCRSTTCGGKDKPLRCDDPRFDDSSSS 145
DB  62 VRFESIRLPGCPGVNPPVSVAVLSCCALCRSTTCGGKDKPLRCDDPRFDDSSSS 121
QY  146 KAPPSLPSPSRPLGSPSDPILPQ 169
DB  122 KAPPSLPSPSRPLGSPSDPILPQ 145

RESULT 13
AAE04491
ID  AAE04491 standard; Protein; 145 AA.
XX
AC  AAE04491;
XX
DT  04-SEP-2001 (first entry)
XX
DE  Human chorionic gonadotropin beta-subunit fragment (1-145 amino acids).
XX
KM  Human; single chain gonadotropin analog; anti-infertility; drug;
KW  peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
KW  FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
XX  glycoprotein; infertility; fusion protein.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  Misc-difference 145
FT  /note= "Residue 'O' is present at this location in the
FT  sequence shown in column 33 of the specification"
XX
PN  US6238890-B1.
XX
PD  29-MAY-2001.
XX
PF  25-AUG-1997; 97US-0918288.
XX
PR  18-FEB-1994; 94US-0199382.
XX  12-AUG-1994; 94US-0289396.
XX  22-SEP-1994; 94US-0310590.
XX  04-NOV-1994; 94US-0334628.
XX  07-DEC-1994; 94US-0351591.
XX  07-JUN-1995; 95US-0475049.
XX  09-MAY-1997; 97US-0853524.
XX
PA  (UNITW ) UNITW WASHINGTON.
XX
PI  Bolme I, Moyle WR;
XX
DR  WPI; 2001-366474/38.
XX
PT  New DNA or RNA encoding single chain protein useful in treating
PT  infertility, as aids in vitro fertilization techniques, or other
PT  therapeutic methods associated with the native hormones.
XX
PS  Example 19; Column 103-106; 87pp; English.
XX
XX  The invention relates to human single chain forms of the glycoprotein
XX  hormone quartet which is an agonist or antagonist of luteinising hormone
XX  (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
XX  (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
XX  having identical alpha subunits and differing beta subunits. The agonist
XX  forms of single chain hormones are used in treating infertility, as aids
XX  in vitro fertilisation techniques, and other therapeutic methods
XX  associated with the native hormones. The single chain hormones are useful
XX  as reagents in a manner similar to heterodimers, as diagnostic tools to
XX  detect the presence of antibodies with respect to the native proteins in
XX  biological samples, as control reagents in assay kits for assessing the
XX  levels of these hormones in various samples, in detecting and purifying
XX  receptors to which the native hormones bind. The single chain hormones
XX  are also used in affinity chromatographic preparation of receptors or

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CC antihormone antibodies. They are used as purification tools for
CC isolation of subsequent preparations of these materials and to monitor
CC levels of single chain hormones administered as drugs. The single chain
CC glycoproteins are used to generate antibodies specifically immunoreactive
CC with these new compounds, as substitutes for the heterodimeric forms of
CC hormones. The present sequence is human chorionic gonadotropin beta-
CC subunit fragment (1-145 amino acids) which is used for constructing
CC single chain gonadotropin analogs related to the invention. Analog
CC fusion proteins serves as useful starting compounds for template directed
CC vaccine design and for the development of hormone-specific vaccines for
CC use in humans.
XX
SQ Sequence 145 AA:

Query Match 80.6%; Score 793; DB 22; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVNCYRD 85
DB 2 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVNCYRD 61

QY 86 VRPESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPITCDPRQDSSSS 145
DB 62 VRPESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPITCDPRQDSSSS 121

QY 146 KAPPSLPSPSRRLPGSPDPTILPQ 169
DB 122 KAPPSLPSPSRRLPGSPDPTILPQ 145

RESULT 14
AAU00709 standard; Protein: 145 AA.
XX
AC AAU00709;
XX
DT 07-SEP-2001 (first entry)
XX
DE Beta-subunit of Human Chorionic Gonadotropin (HCG).
XX
KM Human chorionic gonadotropin beta-subunit; HCG; mammal; pregnancy test;
KM human pituitary luteinizing hormone; reduced fertility; infertility;
KM Contraception; abortion; hormone-associated carcinoma.
XX
OS Homo sapiens.
XX
PN WO200124765-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27741.
XX
PR 06-OCT-1999; 99US-0413564.
XX
PA (OHIS) UNIV OHIO STATE RES FOUND.
XX
PI Stevens VC;
XX
DR WPI; 2001-328306/34.
XX
PT Peptide analogues of beta-human chorionic gonadotropin which are able to
PT raise antibodies against human chorionic gonadotropin are used in
PT vaccines as contraceptives and/or abortifacients -
XX
PS Claim 1; Page 35; 214pp; English.
XX
CC The sequence represents the beta-subunit of human chorionic gonadotropin
CC (betaHCG). Peptide analogues of amino acid residues 38-57 of betaHCG have
CC a disulfide bridge linking the cysteine residues at positions 38 and 57
CC to form a loop structure. The peptides are used in vaccines to raise
CC antibodies against HCG with a significant decrease in antibodies reactive
CC to human pituitary luteinizing hormone, to control the biological

CC activity of endogenous HCG. These antibodies may be used in diagnostic
CC tests to determine hormone levels of mammals. The peptides can be used in
CC pregnancy tests and in detection of reduced fertility or infertility.
CC They may also be administered for contraception or abortion processes.
CC Upon conjugation to a foreign carrier, the peptides may be administered
CC to humans to treat hormone-associated carcinomas.
XX
SQ Sequence 145 AA:

Query Match 80.6%; Score 793; DB 22; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVNCYRD 85
DB 2 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTRVLGVLPAIPQVNCYRD 61

QY 86 VRPESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPITCDPRQDSSSS 145
DB 62 VRPESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPITCDPRQDSSSS 121

QY 146 KAPPSLPSPSRRLPGSPDPTILPQ 169
DB 122 KAPPSLPSPSRRLPGSPDPTILPQ 145

RESULT 15
AAU01139 standard; protein: 145 AA.
XX
AC AAU01139;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human chorionic gonadotropin (HCG) beta-subunit (Structure I).
XX
KM Human chorionic gonadotropin; HCG; contraception; abortion;
KM hormone-related disorder; hormone-associated carcinoma; cancer; diabetes;
KM vascular disease; Zollinger-Ellison syndrome; chronic digestive disorder;
KM antigenic modification.
XX
OS Homo sapiens.
XX
PN US6217881-B1.
XX
PD 17-APR-2001.
XX
PF 06-JUN-1995; 95US-0467997.
XX
PR 06-OCT-1992; 92US-0958601.
PR 07-AUG-1992; 92US-0390530.
PR 04-DEC-1985; 85US-0804642.
PR 17-AUG-1987; 87US-0086401.
XX
PA (OHIS) UNIV OHIO STATE RES FOUND.
XX
PI Stevens VC;
XX
DR WPI; 2001-289819/30.
XX
PT Novel vaccine composition for provoking the formation of antibodies to
PT human chorionic gonadotropin, contains a peptide comprising disulfide
PT bridges linking terminal cysteine residues to form a loop -
XX
PS Disclosure; Column 19; 82pp; English.
XX
CC The present sequence represents the beta-subunit of human chorionic
CC gonadotropin (HCG). The HCG beta-subunit polypeptide sequence is
CC used to isolate 3 novel HCG antigenic peptides (AAU01175-AAU01177)
CC with a disulfide bridge linking the terminal cysteine amino acids
CC to form a loop, and conjugated to a carrier. The HCG antigenic
CC peptides can be used in a vaccine composition for provoking an
CC antibody response to HCG in a mammal. The novel HCG antigenic

CC peptides are useful for the purpose of contraception, abortion,
 CC and for the treatment of hormone-related disease states and
 CC disorders, treatment of hormone-associated carcinomas, and to boost an
 CC animal's resistance to exogenous proteins, such as viral proteins. The
 CC HCG antigenic peptides are also useful for treating cancer, diabetes,
 CC vascular disease, hypertension, Zollinger-Ellison syndrome, and
 CC chronic digestive disorders. Also described are various structures
 CC (AA001140-AA001174) which are non-antigenic, non-endogenous materials
 CC which can be synthetically modified to make them more strongly antigenic,
 CC thereby provoking the formation of relatively large quantities of
 CC antibodies to the non-endogenous materials in the body of the animals,
 CC with consequent reduced risk of damage to the immune system, if exposed
 CC to non-endogenous materials.

XX Sequence 145 AA:

Query Match 80.6%; Score 793; DB 22; Length 145;
 Best Local Similarity 100.0%; Pred. No. 7e-56;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KEPLRRRCRPINATLAVEKEGCPVCITVNTTICAGYCPMTMPVLOGVLPALPQVVCNTRD 85
 |||
 Db 2 KEPLRRRCRPINATLAVEKEGCPVCITVNTTICAGYCPMTMPVLOGVLPALPQVVCNTRD 61
 Qy 86 VRFESIRLPGCRGVNPNVSYAVALSQCACLRSTDCGGPKDHPITCDDPRFQDSSSS 145
 |||
 Db 62 VRFESIRLPGCRGVNPNVSYAVALSQCACLRSTDCGGPKDHPITCDDPRFQDSSSS 121
 Qy 146 KAPPSLPSPSRLLPSPDTPILPQ 169
 |||
 Db 122 KAPPSLPSPSRLLPSPDTPILPQ 145

Search completed: November 20, 2002, 17:27:36
 Job time : 28.8183 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 11.965 Seconds
(without alignments)
1422.126 Million cell updates/sec

Title: US-09-787-494-2

Perfect score: 984

Sequence: 1 MTMTIDSLAVLQRRDMPN.....LPGRSDPRLPQSHNNNNH 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: pirl1:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	793	80.6	165	1 KTHUB	choriogonadotropin
2	785	79.8	145	2 I37231	beta-gonadotropin
3	651	66.2	165	1 KTBAB	choriogonadotropin
4	540	54.9	141	1 UTHUB	lutropin beta chain
5	446	45.3	169	1 KTHOB	choriogonadotropin
6	437	44.4	141	1 UTRBOB	lutropin beta chain
7	437	44.4	141	1 UTRSHB	lutropin beta chain
8	434	44.1	141	1 UTRTB	lutropin beta chain
9	433	44.0	139	2 I52320	testicular lutein
10	427	43.4	119	2 A61465	lutropin beta chain
11	427	43.4	141	1 UTPGB	lutropin beta chain
12	423	43.0	141	1 JC4527	lutropin beta chain
13	420	42.7	138	2 S00512	lutropin beta chain
14	407	41.4	118	2 PN0139	lutropin beta chain
15	406	41.3	118	2 PN0141	lutropin beta chain
16	303	30.8	144	1 UTCAB	gonadotropin beta
17	301	30.6	141	1 B60626	gonadotropin beta
18	301	30.6	146	1 S16763	gonadotropin beta
19	297	30.2	142	2 I51232	gonadotropin II be
20	294	29.9	142	1 C36179	gonadotropin II be
21	280	28.5	142	1 A25800	gonadotropin II be
22	276.5	28.1	113	1 S07092	gonadotropin beta
23	274	27.8	142	2 I50143	gonadotropin II be
24	273	27.3	140	2 A48166	gonadotropin II be
25	269	27.1	128	2 S74085	lutropin beta chain
26	267	26.9	112	2 A61091	lutropin beta chain
27	265	26.9	112	2 S21196	lutropin beta chain
28	258	26.2	166	2 I51242	lutropin beta chain
29	255.5	26.0	80	2 I65235	testicular lutein

ALIGNMENTS

RESULT 1

KTHUB
choriogonadotropin beta chain precursor [validated] - human
N:Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain
C:Species: Homo sapiens (man)
C>Date: 23-Oct-1981 #sequence.revision 23-Oct-1981 #text.change 08-Dec-2000
C:Accession: A93230; 169972; 155224; 155250; 170007; 170008; A92303; A92181; A92142;
R:Riddes, J.C.; Goodman, H.M.
Nature 286, 684-687, 1980
A:Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolu
A:Reference number: A93230; MUID:81012134; PMID:6774259
A:Accession: A93230
A:Molecule type: mRNA
A:Residues: 1-165 <PID>
A:Cross-references: GB:000117; GB:M38559; GB:M54963; NID:g180436; PIDN:AAA96690.1; PI
R:Polliastro, P.; Ovit, C.E.; Hoshina, M.; Fukuoaka, H.; Boothby, M.R.; Boime, I.
J. Biol. Chem. 258, 11492-11499, 1983
A:Title: The beta subunit of human chorionic gonadotropin is encoded by multiple gene
A:Reference number: 155224; MUID:84008141; PMID:6194155
A:Accession: 169972
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-165 <POL>
A:Molecule type: DNA
A:Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453
A:Residues: 1-165 <POL>
A:Molecule type: DNA
A:Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453
A:Accession: 155224
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Cross-references: GB:K03189; NID:g180442; PIDN:AAA53287.1; PID:g180444
A:Note: clone CG-beta-a
R:Polliastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
J. Biol. Chem. 261, 5907-5916, 1986
A:Title: A map of the hCG beta-LH beta gene cluster.
A:Reference number: 155250; MUID:86195987; PMID:2422163
A:Accession: 155250
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <PO3>
A:Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088
A:Note: CG-beta-3 gene
A:Accession: 170007
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <PO4>
A:Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089
A:Note: CG-beta-6 gene
A:Accession: 170008
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090

A>Note: CG-beta-7 gene
 R:Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
 J. Biol. Chem. 256, 1816-1823, 1981
 A:Title: The amino acid sequences of the prepeptides contained in the alpha and beta subunits of human chorionic gonadotropin.
 A:Reference number: A92303; MUID:81117268; PMID:7462224
 A:Accession: A92303
 A:Molecule type: protein
 A:Residues: 1-20 <BIR>
 A>Note: The identity of the residue at position 19 could not be determined
 R:Morgan, F.J.; Birken, S.; Canfield, R.E.
 J. Biol. Chem. 250, 5247-5258, 1975
 A:Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and the beta subunit.
 A:Reference number: A92181; MUID:75211304; PMID:1150658
 A:Accession: A92181
 A:Molecule type: protein
 A:Residues: 21-165 <MOR>
 R:Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
 J. Biol. Chem. 248, 6810-6827, 1973
 A:Reference number: A92142; MUID:74011267; PMID:4795659
 A:Accession: A92142
 A:Molecule type: protein
 A:Residues: 21-22, 'Q', 24-73, 'ZL', 76-140, 142-157, 'PB', 160-165, 'SLP' <CAR>
 R:Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
 Chinese Biochem. J. 6, 558-562, 1990
 A:Title: The immunological characteristics of the enzymatic fragments of human chorionic gonadotropin.
 A:Reference number: PC1016
 A:Accession: PC1016
 A:Molecule type: protein
 A:Residues: 21-165 <SHT>
 A>Note: article in Chinese with English abstract
 R:Birken, S.; Armstrong, E.G.; Kolke, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichewsky, A.; Endocrinology 123, 572-583, 1988
 A:Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pregnancy.
 A:Reference number: A61097; MUID:88254680; PMID:2454811
 A:Accession: A61097
 A:Molecule type: protein
 A:Residues: 26-32, 'X', 34-49, 'X', 51-60, 75-112 <BIR>
 A>Note: this material from pregnancy urine lacks sialic acid in its carbohydrate and has R:Kardana, A.; Bagshaw, K.D.; Coles, B.; Read, D.; Taylor, M.
 B. J. Cancer 67, 686-692, 1993
 A:Title: Characterisation of UCP and its relationship with beta-core fragment.
 A:Reference number: A56873; MUID:93229246; PMID:8471426
 A:Accession: A56873
 A:Molecule type: protein
 A:Residues: 26-28, 'X', 30-32, 'X', 34-42, 'X', 44-45, 'X', 47-48, 75-76, 'X', 78-91, 'G', 93-102 <KA>
 A:Experimental source: urine
 A>Note: sequence modified after extraction from NCBI backbone
 A>Note: this material was designated urinary gonadotropin peptide (peak 2)
 R:Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lusbader, J.W.; Canfield, R.E.; Machin, Nature 369, 455-461, 1994
 A:Title: Crystal structure of human chorionic gonadotropin.
 A:Reference number: A44674; MUID:94261179; PMID:8202136
 A:Contents: annotation: X-ray crystallography, 3.0 angstroms; correction of disulfide bc R:Palmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
 A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin at A:Reference number: 137231; MUID:84093590; PMID:6690982
 A:Accession: 137412
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 21-165 <RES>
 A:Cross-references: EMBL:X00265; NID:931719; PIN:CAA25068.1; PID:q1335075
 C:Genetics:
 A:Gene: GDB:CGR
 A:Cross-references: GDB:119055; OMIM:118860
 A:Map position: 19q13.3-19q13.3
 A:Introns: 5/3; 61/3
 A>Note: the chorionadotropin beta chain locus contains six genes (or pseudogenes)
 C:Keywords: glycoprotein; hormone; pituitary
 F:1-20/Domain: signal sequence #status experimental <SIG>
 F:21-165/Product: chorionadotropin beta chain #status experimental <MAT>
 F:29-77, 43-92, 46-130, 54-108, 58-110, 113-120/Disulfide bonds: #status experimental

F:33,50/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:138,150/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:141,147,152,158/Binding site: carbohydrate (Ser) (covalent) #status experimental
 Query Match 80.6%; Score 793; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 5.6e-56;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 26 KEPLRRCRPNATLAVEKEGCVCTVNTTICAGYCPMTRVLGVPALPOVVCNRYD 85
 |||||||
 DB 22 KEPLRRCRPNATLAVEKEGCVCTVNTTICAGYCPMTRVLGVPALPOVVCNRYD 81
 |||||||
 QY 86 VRFESIRLPDGPGRVNPVSYAVALSQCACLRSTTDCGPKDHPETCDPRFODSSSS 145
 |||||||
 DB 82 VRFESIRLPDGPGRVNPVSYAVALSQCACLRSTTDCGPKDHPETCDPRFODSSSS 141
 |||||||
 QY 146 KAPPSLPSPSRPLPGSDPTPLPQ 169
 |||||||
 DB 142 KAPPSLPSPSRPLPGSDPTPLPQ 165
 |||||||

RESULT 2
 137231
 beta-gonadotropin - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
 C:Accession: 137231
 R:Palmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
 Nature 307, 37-40, 1984
 A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
 A:Reference number: 137231; MUID:84093590; PMID:6690982
 A:Accession: 137231
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-145 <RES>
 A:Cross-references: EMBL:X00266; NID:929907; PIN:CAA25069.1; PID:q1335012
 C:Genetics:
 A:Introns: 41/3
 C:Superfamily: pituitary glycoprotein hormone beta chain
 Query Match 79.8%; Score 785; DB 2; Length 145;
 Best Local Similarity 99.3%; Pred. No. 2.1e-55;
 Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 KEPLRRCRPNATLAVEKEGCVCTVNTTICAGYCPMTRVLGVPALPOVVCNRYD 85
 |||||||
 DB 2 KEPLRRCRPNATLAVEKEGCVCTVNTTICAGYCPMTRVLGVPALPOVVCNRYD 61
 |||||||
 QY 86 VRFESIRLPDGPGRVNPVSYAVALSQCACLRSTTDCGPKDHPETCDPRFODSSSS 145
 |||||||
 DB 62 VRFESIRLPDGPGRVNPVSYAVALSQCACLRSTTDCGPKDHPETCDPRFODSSSS 121
 |||||||
 QY 146 KAPPSLPSPSRPLPGSDPTPLPQ 169
 |||||||
 DB 122 KAPPSLPSPSRPLPGSDPTPLPQ 145
 |||||||

RESULT 3
 KTBAB
 chorionadotropin beta chain precursor - olive baboon
 C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
 C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-May-1999
 C:Accession: A25808
 R:Crawford, R.J.; Tregear, G.W.; Miall, H.D.
 Gene 46, 161-169, 1986
 A:Title: The nucleotide sequences of baboon chorionic gonadotropin beta-subunit genes
 A:Reference number: A25808; MUID:87106851; PMID:2433190
 A:Accession: A25808
 A:Molecule type: mRNA
 A:Residues: 1-165 <CRA>
 A:Cross-references: GB:M14966; NID:q176572; PIN:AAA3383.1; PID:q176573
 C:Comment: There are at least five copies of CG-related genes and at least two of the C:Superfamily: pituitary glycoprotein hormone beta chain

A:Reference number: A5952; MUID:95034847; PMID:7524670
 A:Contents: annotation: glycosylation
 A:Note: horse lutropin and chorionadotropin beta chains have identical protein chains
 C:Superfamily: pituitary glycoprotein hormone beta chain
 C:Keywords: glycoprotein; hormone; pituitary
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-169/Product: lutropin beta chain #status experimental <MAT>
 F:29-77,46-130,54-108,58-110,113-120/Disulfide bonds: #status predicted
 F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 45.3%; Score 446; DB 1; Length 169;
 Best Local Similarity 55.0%; Pred. No. 1,7e-28;
 Matches 88; Conservative 17; Mismatches 41; Indels 14; Gaps 3;

Db 17 WENPCRDLEPRRCRPNATLAVERKPCVCTVNTTTCAGYCPMTWVLOGVLPAL 76
 19 WMSRG-----PLRPLCRPINTLAKEKACICITFTTSTICAGCPSWVRMPALPAI 72
 QY 77 POVCNRYDVRRESIRLPGCPGVNPNVSYAVALSQCQALRRSTDDCGKPDHPLTCD 136
 DB 73 POVCYTHRLRPAVSIRLPGCPGVNPNVSYAVALSCHGCPQIKTTDGCVRFDPLACAP 132

QY 137 PRFODSSSKAPPSLPSPRLPGP-----SDPTLPQPS 171
 DB 133 ----QASSSSKDPSPQPLTSTPTPGASRRSHPIPKTS 169

RESULT 6
 UTROR
 N:Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 24-Nov-1999
 C:Accession: A92534; A92518; A91212; A01499
 R:Vitgin, J.B.; Silver, B.J.; Thomson, A.R.; Nilsson, J.H.
 J. Biol. Chem. 260, 7072-7077, 1985
 A:Title: The gene for the beta subunit of bovine luteinizing hormone encodes a gonadotro
 A:Reference number: A92534; MUID:85207729; PMID:2987241
 A:Accession: A92534
 A:Molecule type: DNA
 A:Residues: 1-141 <VR>
 A:Cross-references: GB:M1506; NID:g163298; PIDN:AMB59267.1; PID:g163299
 R:Maurel, R.A.
 J. Biol. Chem. 260, 4684-4687, 1985
 A:Title: Analysis of several bovine lutropin beta subunit cDNAs reveals heterogeneity in
 A:Reference number: A92518; MUID:85182575; PMID:3838746
 A:Accession: A92518
 A:Molecule type: mRNA
 A:Residues: 3-111, 'S', 113-141 <MAUD>
 A:Cross-references: GB:M10077; NID:g163300; PIDN:AAA30623.1; PID:g163301
 R:Maghuln-Rogister, G.; Hennen, G.
 Eur. J. Biochem. 39, 235-253, 1973
 A:Title: Lutealizing hormone. The primary structures of the beta-subunit from bovine and
 A:Reference number: A91212; MUID:74075724; PMID:4770795
 A:Accession: A91212
 A:Molecule type: Protein
 A:Residues: 21-73, 'E', 75-121, 'PG', 124-125, 'E', 127-139 <MAC>
 A:Note: some carboxyl-terminal heterogeneity was found
 C:Genetics:
 A:Introns: 5/3; 61/3
 C:Superfamily: pituitary glycoprotein hormone beta chain
 C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-141/Product: lutropin beta #status experimental <LTVB>
 F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
 F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
 F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 44.4%; Score 437; DB 1; Length 141;
 Best Local Similarity 61.6%; Pred. No. 7.3e-28;
 Matches 77; Conservative 14; Mismatches 28; Indels 6; Gaps 1;

QY 17 WENPCRDLEPRRCRPNATLAVERKPCVCTVNTTTCAGYCPMTWVLOGVLPAL 76

Db 19 WMSRG-----PLRPLCRPINTLAKEKACICITFTTSTICAGCPSMKRVLPIILP 72
 QY 77 POVCNRYDVRRESIRLPGCPGVNPNVSYAVALSQCQALRRSTDDCGKPDHPLTCD 136
 DB 73 POVCYTHRLRPAVSIRLPGCPGVNPNVSYAVALSCHGCPQLSTDDCGPRTPPLACDH 132

QY 137 PRFOD 141
 DB 133 PPLPD 137

RESULT 7
 UTRSHB
 N:Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 24-Apr-1984 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001
 C:Accession: I46949; S09232; A92110; A90053; B61098; A01500
 R:Brown, P.; McNeilly, J.R.; Wallace, R.M.; McNeilly, A.S.; Clark, A.J.
 Mol. Cell. Endocrinol. 93, 157-165, 1993
 A:Title: Characterization of the ovine LH beta-subunit gene: the promoter directs gon
 A:Reference number: I46949; MUID:93351742; PMID:8349025
 A:Accession: I46949
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-141

 A:Cross-references: GB:S64695; NID:g408240; PIDN:AMB27819.1; PID:g408241
 R:d'Angelo-Bernard, G.; Moumni, M.; Jutisz, M.; Counis, R.
 Nucleic Acids Res. 18, 2175, 1990
 A:Title: Cloning and sequence analysis of the cDNA for the precursor of the beta subu
 A:Reference number: S09232; MUID:90245669; PMID:2336336
 A:Accession: S09232
 A:Molecule type: mRNA
 A:Residues: 1-58, 'L', 60-62, 'Q', 64-141 <ANC>
 A:Cross-references: EMBL:X52486; NID:g1319; PIDN:CA36729.1; PID:g1320
 R:Li, W.K.; Naim, H.S.; Sweeney, C.M.; Holcomb, G.N.; Ward, D.N.
 J. Biol. Chem. 267, 4365-4381, 1992
 A:Title: The primary structure of ovine luteinizing hormone. II. The amino acid sequ
 A:Reference number: A92110; MUID:72211145; PMID:4556309
 A:Accession: A92110
 A:Molecule type: Protein
 A:Residues: 21-121, 'PG', 124-125, 'E', 127-139 <LTV>
 R:Saltram, M.R.; Samy, T.S.A.; Pakroff, H.; Li, C.H.
 Arch. Biochem. Biophys. 153, 572-586, 1972
 A:Title: The primary structure of ovine interstitial cell-stimulating hormone. II. Th
 A:Reference number: A90053; MUID:73190035; PMID:4554535
 A:Accession: A90053
 A:Molecule type: Protein
 A:Residues: 21-29, 'E', 31-71, 'P', 72-80, 'Q', 82-121, 'PG', 124-125, 'E', 127-139 <SAI>
 R:Nomura, K.; Tsunawasa, S.; Ohmura, K.; Sakiyama, F.; Shizume, K.
 Endocrinology 123, 700-712, 1988
 A:Title: Renotropic activity in ovine luteinizing hormone isoform(s).
 A:Reference number: A61098; MUID:88283534; PMID:2456202
 A:Accession: B61098
 A:Molecule type: Protein
 A:Residues: 21-39, 'N', 41-49, 64-78, 'V', 80-82, 84-106, 115-121, 'PG', 124-138 <NOM>
 A:Note: this form was designated form beta-3; forms beta-1 and beta-2 each lack sever
 C:Genetics:
 A:Introns: 5/3; 61/3
 C:Superfamily: pituitary glycoprotein hormone beta chain
 C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-141/Product: lutropin beta chain #status experimental <MAT>
 F:21/Modified site: blocked amino end (Ser) (in mature form) (partial) (probably acet
 F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
 F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 44.4%; Score 437; DB 1; Length 141;
 Best Local Similarity 61.6%; Pred. No. 7.3e-28;
 Matches 77; Conservative 14; Mismatches 28; Indels 6; Gaps 1;

QY 17 WENPCRDLEPRRCRPNATLAVERKPCVCTVNTTTCAGYCPMTWVLOGVLPAL 76

Db 19 WASRG-----PLRPLCRPINATLAERKACPCITFTTSTICAGCPSMKRVLPVLLPMP 72
 Oy 77 POVCNRYDVRPESIRLRGCGPRGVNPNVSYAVALSCOCALCRSTTDCGPKDHPPLTCD 136
 Db 73 PQRVCTYRELRFASVRLPGCGPVDPMVSFPVALSCGCGPCRLSSDCCGPRPQPLACDH 132
 Oy 137 PRFOD 141
 Db 133 PRLPD 137

RESULT 8

luteinizing hormone precursor - rat

N:Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing

C:Species: Rattus norvegicus (Norway rat)

C>Date: 14-Nov-1993 #sequence_revision 14-Nov-1993 #text_change 24-Sep-1999

C:Accession: A01498; P00091; S42527; I83049

R:Jensen, L.; Chin, W.W.; Hollenberg, A.N.; Chang, A.S.; Habener, J.F.

J. Biol. Chem. 259, 15474-15480, 1984

A:Title: The gene encoding the beta-subunit of rat luteinizing hormone. Analysis of gene

A:Reference number: A01498; MUID:85080043; PMID:6096374

A:Accession: A01498

A:Molecule type: DNA

A:Residues: 1-141 <JAN>

A:Cross-references: EMBL:J00749; NID:g205175; PIDN:AAA96703.1; PID:g205176

R:Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.

submitted to JIPD, July 1990

A:Reference number: P00091

A:Accession: P00091

A:Molecule type: mRNA

A:Residues: 4-141 <KAT>

R:Chin, W.W.; Godine, J.E.; Klein, D.R.; Chang, A.S.; Tan, L.K.; Habener, J.F.

Proc. Natl. Acad. Sci. U.S.A. 80, 4649-4653, 1983

A:Title: Nucleotide sequence of the cDNA encoding the precursor of the beta subunit of

A:Reference number: S42527; MUID:83273673; PMID:6192440

A:Accession: S42527

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-141 <CHT>

A:Cross-references: GB:J00749; GB:M54957; NID:g205175; PIDN:AAA96703.1; PID:g205176

R:Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.

Zool. Sci. 7, 879-887, 1990

A:Title: Strain Difference in Nucleotide Sequences of Rat Glycoprotein Hormone Subunit C

A:Reference number: I60104

A:Accession: I83049

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 4-141 <RES>

A:Cross-references: GB:D00576; NID:g220807; PIDN:BA00454.1; PID:g220808

C:Comment: The beta chain confers the specificity of the hormone.

C:Genetics:

A:Introns: 5/3; 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: glycoprotein; hormone; pituitary

F:1-21/Omim: signal sequence #status predicted <SIG>

F:22-14/Product: luteinizing hormone #status predicted <LMB>

F:29-54,43-77,46-108,130-92,120,110-113/Disulfide bonds: #status predicted

F:33/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 44.1%; Score 434; DB 1; Length 141;

Best Local Similarity 62.0%; Pred. No. 1.3e-27;

Matches 75; Conservative 16; Mismatches 24; Indels 6; Gaps 1;

Oy 17 WENPGCRDLKEPLRRCRPIINATLAVERGECPCITVNTTICAGCPTMTRVLGVLPAAL 76
 Db 19 WASRG-----PLRPLCRPVNATLAENEFPCVCTFTTSTICAGCPSMVRVLPALPVP 72
 Oy 77 POVCNRYDVRPESIRLRGCGPRGVNPNVSYAVALSCOCALCRSTTDCGPKDHPPLTCD 136
 Db 73 PQRVCTYRELRFASVRLPGCGPVDPMVSFPVALSCGCGPCRLSSDCCGPRPQPLACDH 132

Oy 137 P 137
 Db 133 P 133

RESULT 9

testicular luteinizing hormone beta-subunit - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999

C:Accession: I52320

R:Zhang, F.P.; Kannikko, A.; Huhtaniemi, I.

Biochem. Biophys. Res. Commun. 210, 858-865, 1995

A:Title: Isolation and characterization of testis-specific cDNAs for luteinizing horm

A:Reference number: I52320; MUID:95283549; PMID:7763258

A:Accession: I52320

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-139 <RES>

A:Cross-references: EMBL:U25653; NID:g915216; PIDN:AAC52249.1; PID:g915217

C:Genetics:

A:Gene: TLHB1

C:Superfamily: pituitary glycoprotein hormone beta chain

Query Match 44.0%; Score 433; DB 2; Length 139;

Best Local Similarity 61.2%; Pred. No. 1.5e-27;

Matches 74; Conservative 17; Mismatches 24; Indels 6; Gaps 1;

Oy 17 WENPGCRDLKEPLRRCRPIINATLAVERGECPCITVNTTICAGCPTMTRVLGVLPAAL 76
 Db 17 WASRG-----PLRPLCRPVNATLAENEFPCVCTFTTSTICAGCPSMVRVLPALPVP 70
 Oy 77 POVCNRYDVRPESIRLRGCGPRGVNPNVSYAVALSCOCALCRSTTDCGPKDHPPLTCD 136
 Db 71 PQRVCTYRELRFASVRLPGCGPVDPMVSFPVALSCGCGPCRLSSDCCGPRPQPLACDH 130

Oy 137 P 137
 Db 131 P 131

RESULT 10

lutropin beta chain - rabbit

A:Accession: A61465

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-1995

C:Accession: A61465

R:Glenn, S.D.; Naim, H.S.; Ward, D.N.

J. Protein Chem. 3, 259-273, 1984

A:Title: The amino acid sequence of the rabbit lutropin beta subunit.

A:Reference number: A61465

A:Accession: A61465

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-119 <GLE>

A>Note: the sequence from Fig. 1 is inconsistent with that from the abstract in havin

C:Superfamily: pituitary glycoprotein hormone beta chain

F:11-36,25-59,28-90,40-112,74-102,92-95/Disulfide bonds: #status predicted

Query Match 43.4%; Score 427; DB 2; Length 119;

Best Local Similarity 67.3%; Pred. No. 3.8e-27;

Matches 74; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

Oy 28 PLRPGCRPIINATLAVERGECPCITVNTTICAGCPTMTRVLGVLPAALPOVCNRYDVR 87
 Db 6 PLRPLCRPVNATLAENEFPCVCTFTTSTICAGCPSMVRVLPALPVPQPVCTYREL 65
 Oy 88 FESIRLPGCGPRGVNPNVSYAVALSCOCALCRSTTDCGPKDHPPLTCD 137
 Db 66 FASIRLPGCGPVDPMVSFPVALSCGCGPCRLSSDCCGPRPQPLACDH 115

RESULT 11

UTRPG8

Luteolin beta chain precursor - pig

N:Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing hormone (LH) beta chain; luteinizing hormone (LH) beta chain

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000

R:Accession: A48170; A50322; A01501; A60584

J:MOI: Endocrinol. 5, 137-146, 1990

A:Title: The gene for the beta subunit of porcine LH: clusters of GC boxes and CACCC elements

A:Reference number: A48170; MUID:91063934; PMID:1701088

A:Accession: A48170

A:Molecule type: DNA

A:Residues: 1-141 <EZA>

A:Cross-references: GB:D00579; NID:9217693; PIDN:BA00457.1; PID:9217694

Mol. Cell. Endocrinol. 62, 47-53, 1989

A:Title: Cloning and DNA sequence analysis of the cDNA for the precursor of porcine luteinizing hormone

A:Reference number: A50322; MUID:89306142; PMID:2744222

A:Accession: A50322

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-141 <KAT>

R:Maghni-Rogister, G.; Hennen, G.

Eur. J. Biochem. 39, 235-253, 1973

A:Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and porcine

A:Reference number: A91212; MUID:74075724; PMID:4770795

A:Accession: A01501

A:Molecule type: protein

A:Residues: 21-29, '2', '31-39, 'D', '41-61, 'R', '63-82, 'I', '84-86, 'S', '88-121, 'PG', '124-133, 'P', '134-141

A:Note: 30-AAG was also found

A:Note: about half the chains lack one or both carboxyl-terminal leucines

R:Nomura, K.; Ohmura, K.; Nakamura, Y.; Horiba, N.; Shirakura, Y.; Sato, Y.; Ujihara, M.

Endocrinology 124, 712-719, 1989

A:Title: Porcine luteinizing hormone isoform(s): relationship between their molecular structure and biological activity

A:Reference number: A60584; MUID:89107050; PMID:2356317

A:Accession: A60584

A:Molecule type: protein

A:Residues: 21-31; 137-139 <NOM>

A:Note: the luteolin beta chain is heterogeneous at the carboxyl end; this form lacked the

A:Gene(s):

A:Introns: 5/3; 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: blocked amino end; glycoprotein; hormone

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-141/Product: luteolin beta chain #status experimental <MAT>

F:23-54, 43-77, 46-108, 58-130, 92-120, 110-113/Disulfide bonds: #status predicted

F:33/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match

Best Local Similarity 43.4%; Score 427; DB 1; Length 141;

Matches 76; Conservative 11; Mismatches 28; Indels 6; Gaps 1;

QY 17 WENPGCRDLKEPLRRCRPNATLAVERGECPCVITVTTCAGCPTMTVRLGVLPAL 76

Db 19 WASRG-----PLRPLCRPNATLAENEFPCVITVTTCAGCPTMTVRLGVLPAL 76

QY 77 PQVNCNRDVRERESIRLPGCPGPNVSVAVALSOCALCRSTTDCGGKDPHPLTCD 136

Db 73 PQVCTYHELFASIRLPGCPGPNVSVAVALSOCALCRSTTDCGGKDPHPLTCD 136

Gene 166, 335-336, 1995

A:Title: Cloning of the mouse gonadotropin beta-subunit-encoding genes, II. Structure

A:Reference number: J04527; MUID:96125216; PMID:8543188

A:Accession: J04527

A:Molecule type: mRNA

A:Residues: 1-141 <KUM>

A:Cross-references: GB:U25145; NID:9930344; PIDN:AAA2841.1; PID:9930345

A:Experimental source: 1295YEV

C:Comment: This protein is co-produced with follicle-stimulating hormone in pituitary

n reproduction including gonadal growth, gametogenesis and steroidogenesis.

A:Gene(s): lh beta

A:Introns: 5/3; 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: hormone; reproduction

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-141/Product: luteinizing hormone beta chain #status predicted <MAT>

Query Match

Best Local Similarity 43.0%; Score 423; DB 2; Length 141;

Matches 73; Conservative 16; Mismatches 26; Indels 6; Gaps 1;

QY 17 WENPGCRDLKEPLRRCRPNATLAVERGECPCVITVTTCAGCPTMTVRLGVLPAL 76

Db 19 WASRG-----PLRPLCRPNATLAENEFPCVITVTTCAGCPTMTVRLGVLPAL 76

QY 77 PQVNCNRDVRERESIRLPGCPGPNVSVAVALSOCALCRSTTDCGGKDPHPLTCD 136

Db 73 PQVCTYHELFASIRLPGCPGPNVSVAVALSOCALCRSTTDCGGKDPHPLTCD 136

QY 137 P 137

Db 133 P 133

RESULT 13

Luteolin beta chain precursor - dog (fragment)

N:Alternate names: luteinizing hormone beta chain

C:Species: Canis lupus familiaris (dog)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

R:Accession: S00512

R:Wolf, D.L.; Appleby, V.L.; Hjertild, K.; Baker, A.R.; Talmadge, K.

Nucleic Acids Res. 15, 10602, 1987

A:Title: Nucleic acid and amino acid sequences of dog beta-LH: comparison to rat, cow

A:Reference number: S00512; MUID:88096605; PMID:3697104

A:Accession: S00512

A:Molecule type: mRNA

A:Residues: 1-138 <WOL>

A:Cross-references: EMBL:X00518; NID:9907; PIDN:CAA6857.1; PID:9860906

C:Superfamily: pituitary glycoprotein hormone beta chain

F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>

F:18-138/Product: luteolin beta chain #status predicted <MAT>

F:26-51, 40-74, 43-105, 55-127, 89-117, 107-110/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 42.7%; Score 420; DB 2; Length 138;

Matches 75; Conservative 11; Mismatches 29; Indels 6; Gaps 1;

QY 17 WENPGCRDLKEPLRRCRPNATLAVERGECPCVITVTTCAGCPTMTVRLGVLPAL 76

Db 16 WASRG-----PLRPLCRPNATLAENEFPCVITVTTCAGCPTMTVRLGVLPAL 76

QY 77 PQVNCNRDVRERESIRLPGCPGPNVSVAVALSOCALCRSTTDCGGKDPHPLTCD 136

Db 70 PQVCTYHELFASIRLPGCPGPNVSVAVALSOCALCRSTTDCGGKDPHPLTCD 136

QY 137 P 137

Db 130 P 130

RESULT 14

Luteinizing hormone beta chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 16-Jul-1999

R:Accession: J04527

R:Kumar, T.R.; Matzuk, M.M.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:26 ; Search time 7.01399 Seconds
(without alignments)
1046.667 Million cell updates/sec

Title: US-09-787-494-2

Perfect score: 984

Sequence: 1 MFWITDLSAVLQRRWENP.....LPSPDPRLPQTSNNHHHH 177

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	793	80.6	165	1	CGHB_HUMAN
2	651	66.2	165	1	CGHB_PAPAN
3	540	54.9	141	1	LSHB_HUMAN
4	516.5	52.5	164	1	CGHB_CALJA
5	476	48.4	169	1	LSHB_EOUBU
6	461	46.8	169	1	LSHB_EOUBU
7	446	45.3	169	1	LSHB_HORSE
8	444	45.1	143	1	LSHB_FELCA
9	437	44.4	141	1	LSHB_BOVIN
10	434	44.1	141	1	LSHB_RAT
11	428	43.5	141	1	LSHB_CERSI
12	427	43.4	141	1	LSHB_PIG
13	427	43.4	141	1	LSHB_SHEEP
14	423	43.0	141	1	LSHB_MOUSE
15	420	42.7	138	1	LSHB_CANFA
16	407	41.4	118	1	LSHB_BALAC
17	407	41.4	128	1	LSHB_PHOSU
18	406	41.3	118	1	LSHB_PHYCA
19	405.5	41.2	138	1	LSHB_MACRU
20	393	39.9	141	1	LSHB_TRIYU
21	303	30.8	140	1	GTH2_CARAU
22	303	30.8	144	1	GTH2_HYPMO
23	301	30.6	141	1	GTH2_CTEID
24	301	30.6	146	1	GTH2_ONCMA
25	297	30.2	142	1	GTH2_ONCMA
26	294	29.9	142	1	GTH2_ONCMA
27	284	28.9	140	1	GTH2_ICTPU
28	283	28.8	138	1	GTH2_ICTPU
29	282	28.7	149	1	GTH2_CLUGA
30	280	28.5	142	1	GTH2_ONCMA
31	276.5	28.1	113	1	GTHB_MURCI
32	274	27.8	142	1	GTH2_CORAU
33	273	27.7	140	1	GTH2_ANGAN

34	269	27.3	128	1	LSHB_STRCA	P80664 struthio ca
35	265	26.9	112	1	LSHB_RANCA	P80071 rana catesb
36	258	26.2	166	1	LSHB_COTJA	P45657 coturnix co
37	257	26.1	137	1	GTH2_ACALA	O90225 acanthopagr
38	255.5	26.0	132	1	GTH1_ICTPU	O9d681 ictalurus p
39	255	25.9	139	1	GTH2_MORSA	O91121 morone saxa
40	255	25.9	146	1	GTH2_TRITC	O9pw98 trichogaste
41	255	25.9	159	1	LSHB_MELGA	P45646 meleagris g
42	254	25.8	127	1	GTH1_ANGJA	O9y9k3 anguilla ja
43	254	25.8	138	1	LSHB_CANFA	P54828 canis famil
44	252	25.6	115	1	GTH2_THUOB	P37206 thunnus obe
45	243	24.7	138	1	LSHB_BOVIN	P01223 bos taurus

ALIGNMENTS

RESULT 1
ID CGHB_HUMAN STANDARD: PRT; 165 AA.
AC P01233; Q14000; Q13991;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Choriogonadotropin beta chain precursor (Chorionic gonadotropin beta
subunit) (CG-beta).
GN GCB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed-6774259;
RA MEDLINE=81012134.
RT Fiddes J.C., Goodman H.M.;
RT "The cDNA for the beta-subunit of human chorionic gonadotropin
suggests evolution of a gene by readthrough into the 3'-untranslated
region.";
RL Nature 286:684-687(1980).
RN [2]
RP SEQUENCE FROM N.A. PubMed-6690982;
RA MEDLINE=84093590.
RT Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT "Evolution of the genes for the beta subunits of human chorionic
gonadotropin and luteinizing hormone.";
RL Nature 307:37-40(1984).
RN [3]
RP SEQUENCE FROM N.A. PubMed-6194155;
RA MEDLINE=84008141.
RT Policastro P., Ovitc C.E., Hoshina M., Fukuoaka H., Boothby M.R.,
RA Boime I.;
RT "The beta subunit of human chorionic gonadotropin is encoded by
multiple genes.";
RL J. Biol. Chem. 256:11492-11499(1983).
RN [4]
RP SEQUENCE OF 1-20.
RA MEDLINE=81117268; PubMed-7462224;
RT Birken S., Featherston J., Canfield R.E., Boime I.;
RT "The amino acid sequences of the prepeptides contained in the alpha
and beta subunits of human chorionic gonadotropin.";
RL J. Biol. Chem. 256:1816-1823(1981).
RN [5]
RP SEQUENCE OF 21-165.
RA MEDLINE=7521304; PubMed-1150658;
RT Morgan F.J., Birken S., Canfield R.E.;
RT "The amino acid sequence of human chorionic gonadotropin. The alpha
subunit and beta subunit.";
RL J. Biol. Chem. 250:5247-5258(1975).
RN [6]
RP PRELIMINARY SEQUENCE OF 21-165.
RA MEDLINE=74011267; PubMed-4795659;
RT Carlsen R.B., Bahl O.P., Swaminathan N.;
RT "Human chorionic gonadotropin. Linear amino acid sequence of the beta

RT subunit.";
 RL J. Biol. Chem. 248:6810-6827(1973).
 RN [7]
 RN SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=66195987; PubMed=2422163;
 RA Policastro P.F., Daniels-McQueen S., Carle G., Bolme I.;
 RT "A map of the hCG beta-LH beta gene cluster.";
 RL J. Biol. Chem. 261:5907-5916(1986).
 RN [8]
 RN PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
 RX MEDLINE=81215630; PubMed=7240231;
 RA Mise T., Bahl O.P.;
 RT "Assignment of disulfide bonds in the beta subunit of human chorionic
 gonadotropin.";
 RL J. Biol. Chem. 256:6587-6592(1981).
 RN [9]
 RN DISULFIDE BONDS.
 RX MEDLINE=90094415; PubMed=1688430;
 RA Saccuzo Beebe J., MountJoy K., Krzeslcki R.F., Perini F.,
 RA Rudon R.W.;
 RT "Role of disulfide bond formation in the folding of human chorionic
 gonadotropin beta subunit into an alpha beta dimer assembly-competent
 form.";
 RL J. Biol. Chem. 265:312-317(1990).
 RN [10]
 RN STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=92314469; PubMed=1820200;
 RA Weisshaar G., Hiyama J., Renwick A.G.C.;
 RT "Site-specific N-glycosylation of human chorionic gonadotropin --
 structural analysis of glycopeptides by one- and two-dimensional 1H
 NMR spectroscopy.";
 RL Glycobiology 1:393-404(1991).
 RN [11]
 RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=94261179; PubMed=8202136;
 RA Lepthorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,
 RA Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;
 RT "Crystal structure of human chorionic gonadotropin.";
 RL Nature 369:455-461(1994).
 CC -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
 ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
 CC -1- SUBUNIT: HETERO DIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -1- TISSUE SPECIFICITY: PLACENTA.
 CC -1- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
 CC -1- PHARMACEUTICAL: Available under the names Novarel (Ferring) and
 Profasi (Serono).
 CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 FAMILY.
 CC -----
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 DR EMBL: J00117; AAA96690.1; -;
 DR EMBL: X00265; CAA25068.1; ALT_INIT.
 DR EMBL: X00266; CAA25069.1; ALT_INIT.
 DR EMBL: M13504; AAA52005.1; -;
 DR EMBL: M13505; AAA52008.1; -;
 DR EMBL: M13503; AAA52009.1; -;
 DR EMBL: K03189; AAA53288.1; -;
 DR EMBL: K03187; AAA53288.1; JOINED.
 DR EMBL: K03188; AAA53287.1; JOINED.
 DR EMBL: K00092; AAA53287.1; JOINED.
 DR EMBL: K03182; AAA53287.1; JOINED.
 DR PIR: A01502; KTHUB.
 DR PDB: 1HCN; 30-SEP-94.

DR PDB: 1HRP; 01-NOV-94.
 DR PDB: 1XUL; 15-MAY-97.
 DR GlycoSitedb; P01233; -;
 DR Genew; HGNC:1886; CGB.
 DR Genew; HGNC:16451; CGB7.
 DR Genew; HGNC:16452; CGB5.
 DR MIM; 118860; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001545; Gly_hormoneb.
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 DR KW Hormone; Glycoprotein; Signal; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 20
 FT CHAIN 21 165
 FT DISULFID 29 77
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT DISULFID 54 108
 FT DISULFID 58 110
 FT DISULFID 113 120
 FT CARBOHYD 33 33
 FT CARBOHYD 50 50
 FT CARBOHYD 141 141
 FT CARBOHYD 147 147
 FT CARBOHYD 152 152
 FT CARBOHYD 158 158
 FT VARIANT 137 137
 FT CONFLICT 24 24
 FT SEQUENCE 165 AA; 17739 MM; 5596B9B5E1A05748 CRC64;
 SQ
 Query Match 80.6%; Score 793; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 7; le-60;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 26 KEPLRPKCRPTNATLAVEKESCPYCVITVNTTICAGCPMTRVLYGVLPAIPQVVCYKRD 85
 DB 22 KEPLRPKCRPTNATLAVEKECCPCIVNTTICAGCPMTRVLYGVLPAIPQVVCYKRD 81
 QY 86 VRFESIRLPQCPGVNPNVSYAVALSCCALCRSTTDCGPKDPPTCDPRFQDSSSS 145
 DB 82 VRFESIRLPQCPGVNPNVSYAVALSCCALCRSTTDCGPKDPPTCDPRFQDSSSS 141
 QY 146 KAPPSLSPSPRLPGPSDPTLPQ 169
 DB 142 KAPPSLSPSPRLPGPSDPTLPQ 165
 ID CGB_PAPAN STANDARD; PRT; 165 AA.
 AC P07434;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Choriongonadotropin beta chain precursor (Chorionic gonadotropin beta
 subunit) (CG-beta).
 GN CGB.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 ON NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=67106851; PubMed=2433190;
 RA Crawford R.J., Tregear G.W., Niall H.D.;

```

RT  "The nucleotide sequences of baboon chorionic gonadotropin
RT  beta-subunit genes have diverged from the human."
CC  RT  Gene 46:161-169(1986).
CC  -I- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC  ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY
CC  -I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC  CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC  LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC  -I- TISSUE SPECIFICITY: PLACENTA.
CC  -I- MISCELLANEOUS: THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES
CC  AND AT LEAST TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
CC  -I- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC  FAMILY.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: M14966; AAA35383.1; -.
DR  PIR: A25808; KTBA.
DR  HSSP: P01233; LXDL.
DR  InterPro: IPR000359; Cys_knot.
DR  InterPro: IPR002400; GF_cyskn.
DR  InterPro: IPR001545; Gly_hormoneb.
DR  Pfam: PF00007; Cys_knot.1.
DR  PRINTS: PR00438; GFCSKNOT.
DR  SMART: SM00068; GH.1.
DR  PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR  PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
DR  Hormone: Glycoprotein; Signal.
FT  SIGNAL 1 20 BY SIMILARITY.
FT  CHAIN 1 165 CHORIOGONADOTROPIN BETA CHAIN.
FT  DISULFID 29 77 BY SIMILARITY.
FT  DISULFID 46 92 BY SIMILARITY.
FT  DISULFID 43 130 BY SIMILARITY.
FT  DISULFID 54 108 BY SIMILARITY.
FT  DISULFID 58 110 BY SIMILARITY.
FT  DISULFID 113 120 BY SIMILARITY.
FT  CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT  CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT  CARBOHYD 141 141 O-LINKED (BY SIMILARITY).
FT  CARBOHYD 147 147 O-LINKED (BY SIMILARITY).
FT  CARBOHYD 152 152 O-LINKED (BY SIMILARITY).
SQ  SEQUENCE 165 AA: 17592 MW: 36D3E207A9F1E1C3 CRC64;

Query Match 66.2%; Score 651; DB 1; Length 165;
Best Local Similarity 79.2%; Pred. No. 5,4e-48;
Matches 118; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

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DE  Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LH-
DE  beta) (LH-B) (LH-B).
GN  LHB.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX  NCBI_TaxID=9606;
RX  MEDLINE=76062547; PubMed=1191677;
RX  MEDLINE=84093590; PubMed=6690982;
RX  Talmadge K., Vamvakopoulos N.C., Fildes J.C.;
RT  "Evolution of the genes for the beta subunits of human chorionic
RT  gonadotropin and luteinizing hormone."
RT  Nature 307:37-40(1984).
RN  [12]
RN  SEQUENCE OF 21-141.
RP  MEDLINE=76062547; PubMed=1191677;
RA  Saitam M.R., Li C.H.;
RT  "Human pituitary lutropin. Isolation, properties, and the complete
RT  amino acid sequence of the beta-subunit."
RL  Blochim. Biophys. Acta 412:70-81(1975).
RN  [13]
RN  PRELIMINARY SEQUENCE OF 21-141.
RP  MEDLINE=73090987; PubMed=4685398;
RA  Shome B., Parlow A.F.;
RT  "The primary structure of the hormone-specific, beta subunit of human
RT  pituitary luteinizing hormone (hLH)."
RL  J. Clin. Endocrinol. Metab. 36:618-621(1973).
RN  [14]
RN  PRELIMINARY PARTIAL SEQUENCE.
RP  MEDLINE=73221227; PubMed=4719207;
RA  Closset J., Hennem G., Leguin R.M.;
RT  "Human luteinizing hormone. The amino acid sequence of the
RT  subunit."
RL  FEBS Lett. 29:97-100(1973).
RN  [15]
RN  STRUCTURE OF CARBOHYDRATE.
RP  MEDLINE=91122088; PubMed=1991473;
RA  Weisshaar G., Hiyama J., Renwick A.G.C., Nimtz M.;
RT  "NMR investigations of the N-linked oligosaccharides at individual
RT  glycosylation sites of human lutropin."
RL  Eur. J. Biochem. 195:257-268(1991).
RN  [16]
RN  STRUCTURE BY NMR OF 58-77.
RP  MEDLINE=92357029; PubMed=1495492;
RA  Keutmann H.T., Hua O.-X., Weiss M.A.;
RT  "Structure of a receptor-binding fragment from human luteinizing
RT  hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
RT  resonance spectroscopy."
RL  Mol. Endocrinol. 6:904-913(1992).
RN  [17]
RN  VARIANT ARG-74.
RP  MEDLINE=92085985; PubMed=1727547;
RA  Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
RT  Jameson J.L.;
RT  "Hypogonadism caused by a single amino acid substitution in the beta
RT  subunit of luteinizing hormone."
RL  New Engl. J. Med. 326:179-183(1992).
RN  [18]
RN  FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
RN  THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
RN  -I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
RN  CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
RN  LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
RN  -I- TISSUE SPECIFICITY: PITUITARY.
RN  -I- CHARACTERIZED BY INFERTILITY AND PSEUDOHYPADRODITISM.
RN  -I- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
RN  FAMILY.
RN  -----
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DR EMBL: X00264; CA25067.1; - ALT_SEQ.
 DR EMBL: S71273; AADI4960.1; ALT_SEQ.
 DR PIR: A01457; UTHUB.
 DR HSSP: P01233; 1XUL.
 DR GlysultedB: P01229; -
 DR Genew: HGNC:6584; LHB.
 DR MIM: 152780; -
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR002400; GE_cysknot.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR Pfam: PF00007; Cys_knot; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
 DR Hormone; Glycoprotein; Signal; Pseudothermaphroditism;
 KW Disease mutation.
 FT SIGNAL 1 20
 FT CHAIN 21 141
 FT DISULFID 29 77
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT DISULFID 54 108
 FT DISULFID 58 110
 FT DISULFID 113 120
 FT CARBOHYD 50 50
 FT VARIANT 74 74
 FT FT
 FT CONFLICT 39 39
 FT CONFLICT 76 76
 FT CONFLICT 132 135
 FT SEQUENCE 141 AA; 15345 MW; E411766253113F7C CRC64;
 SQ SEQUENCE

Query Match 54.9%; Score 540; DB 1; Length 141;
 Best Local Similarity 85.0%; Pred. No. 9e-39;
 Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 26 KEPLRPRCPINATLAVERGCPVCITVNTTICAGCPTMTVRLQGVLPALPQVVCYRD 85
 Db 22 KEPLRPRCPINATLAVERGCPVCITVNTTICAGCPTMTVRLQGVLPALPQVVCYRD 81
 QY 86 VREFSIRLPCCRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPR 138
 Db 82 VREFSIRLPCCRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPR 134

RESULT 4
 CGHB_CALJA STANDARD; PRT; 164 AA.
 ID CGHB_CALJA
 AC P51500;
 DT 01-OCT-1996 (Rel. 34; Created)
 DT 01-OCT-1996 (Rel. 34; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Chorionadotropin beta chain precursor (Chorionic gonadotropin beta subunit) (CG-beta).
 GN CGB.
 OS Callithrix jacchus (Chordata: Mammalia: Euteleostomi: Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Platyrrhini: Callitrichidae: Callitrix.
 OC NCBI_TaxID=9483;
 OX NCBI_TaxID=9483;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96115012; PubMed=7492691;
 RA Simila A.P., Amato F., Faast R., Lopata A., Berka J., Norman R.J.;
 "Lutealizing hormone/chorionic gonadotropin bioactivity in the common

marmoset (Callithrix jacchus) is due to a chorionic gonadotropin molecule with a structure intermediate between human chorionic gonadotropin and human luteinizing hormone.";
 RL Biol. Reprod. 53:380-389(1995).
 CC -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -1- TISSUE SPECIFICITY: PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
 CC -----
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DR EMBL: U04447; AAC00029.1; -
 DR HSSP: P01233; 1XUL.
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR002400; GE_cysknot.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR Pfam: PF00007; Cys_knot; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
 DR Hormone; Glycoprotein; Signal
 FT SIGNAL 1 20
 FT CHAIN 21 164
 FT DISULFID 29 77
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT DISULFID 54 108
 FT DISULFID 58 110
 FT DISULFID 113 120
 FT CARBOHYD 50 50
 FT CARBOHYD 146 146
 FT CARBOHYD 151 151
 FT SEQUENCE 164 AA; 17712 MW; 0CD92EDDC2618FA6 CRC64;
 SQ SEQUENCE

Query Match 52.5%; Score 516.5; DB 1; Length 164;
 Best Local Similarity 66.0%; Pred. No. 9.7e-37;
 Matches 95; Conservative 17; Mismatches 31; Indels 1; Gaps 1;

QY 26 KEPLRPRCPINATLAVERGCPVCITVNTTICAGCPTMTVRLQGVLPALPQVVCYRD 85
 Db 22 KEPLRPRCPINATLAVERGCPVCITVNTTICAGCPTMTVRLQGVLPALPQVVCYRD 81
 QY 86 VREFSIRLPCCRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPR 145
 Db 82 LFTSVIRLPCCRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPR 140
 QY 146 KAPPSLPSPRLPSPDPIPQ 169
 Db 141 KDPSPRLPSPSLPDPPIPQ 164

RESULT 5
 LSHB_EOUBU STANDARD; PRT; 169 AA.
 ID LSHB_EOUBU
 AC O46641;
 DT 15-DEC-1998 (Rel. 37; Created)
 DT 15-DEC-1998 (Rel. 37; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Lutropin/chorionadotropin beta chain precursor (LSH-B/CG-B) (luteinizing hormone beta subunit).
 GN LHB.
 OS Equus burchelli (Plains zebra) (Equus quagga).


```

GN LHB
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pituitary;
RA Pukazhentli B.S., Varma G.M., Brown J.L.;
RT "Molecular cloning and sequence analysis of the cDNA for the feline
RT luteinizing hormone beta subunit.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
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CC -----
DR EMBL: AF095716; AAC64196.1; -.
DR HSSP: P01233; 1XUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR001545; Gly_hormoneB.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone: Signal; Glycoprotein.
FT SIGNAL 1 22
FT CHAIN 23 143 LUTROPIN BETA CHAIN.
FT DISULFID 31 79 BY SIMILARITY.
FT DISULFID 45 94 BY SIMILARITY.
FT DISULFID 48 132 BY SIMILARITY.
FT DISULFID 56 110 BY SIMILARITY.
FT DISULFID 60 112 BY SIMILARITY.
FT DISULFID 115 122 BY SIMILARITY.
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 143 AA; 15318 MW; C5C55DDC907422DB CRC64;

Query Match 45.1%; Score 444; DB 1; Length 143;
Best Local Similarity 67.9%; Pred. No. 9..9e-31;
Matches 76; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 26 KEPLRPRCPINATLAVEEGCPVCTVTTCAGCPTMTRYLQGVLDALPOVVCNRYD 85
DB 24 REPLRLCPRIATLAENACPVCTFTTTCAGCPSMMRLPALPVPDPVCTYRE 83
QY 86 VFEESIRLFCRGVNVSVYVALSCCCLCRSTTDCGPGPDHLCTDDP 137
DB 84 LRFASVRLPGCPGVDVPSFVALSCRCGPCRLSSDCCGGAPADPLACDRP 135

RESULT 9
LSHB_BOVIN
ID LSHB_BOVIN STANDARD; PRT; 141 AA.
AC P04651;
DT 13-AUG-1987 (rel. 05, Created)
DT 01-JAN-1988 (rel. 06, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
LHB.

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OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85207729; PubMed=2987241;
RA Virgin J.B., Silver B.J., Thomson A.R., Nilson J.H.;
RT "The gene for the beta subunit of bovine luteinizing hormone encodes
RT a gonadotropin mRNA with an unusually short 5'-untranslated region.";
RL J. Biol. Chem. 260:7072-7077(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85182575; PubMed=3838746;
RA Maurer R.A.;
RT "Analysis of several bovine lutropin beta subunit cDNAs reveals
RT heterogeneity in nucleotide sequence.";
RL J. Biol. Chem. 260:4684-4687(1985).
RN [3]
RP SEQUENCE OF 21-139.
RX MEDLINE=74075724; PubMed=4770795;
RA Maguin-Rogister G., Hennen G.;
RT "Luteinizing hormone. The primary structures of the beta-subunit from
RT bovine and porcine species.";
RL Eur. J. Biochem. 39:235-253(1973).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M10077; AAA30623.1; -.
DR EMBL: M11506; AAB59267.1; -.
DR PIR: A01499; 1XUL.
DR HSSP: P01233; 1XUL.
DR GlycoSuiteDB: P04651; -.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR001545; Gly_hormoneB.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone: Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).
FT FTID=CAR_000044.
FT MISSING (IN REF. 2).
FT CONFLICT 74 74 Q -> E (IN REF. 3).
FT CONFLICT 112 112 P -> S (IN REF. 2).
FT CONFLICT 122 123 GP -> PG (IN REF. 3).
FT CONFLICT 126 126 Q -> E (IN REF. 3).
SQ SEQUENCE 141 AA; 15202 MW; 44FB1CBA4901BC95 CRC64;

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Query Match 44.48; Score 437; DB 1; Length 141;
 Best Local Similarity 61.0%; Pred. No. 3.8e-30;
 Matches 77; Conservative 14; Mismatches 28; Indels 6; Gaps 1;

17 WENGRCDLKEPRPCRPINATLAVEKEGCPVITNTTCAGCPTMRVLOGVLPAL 76
 19 WASRG-----PLRPLCPINATLAEKEKCPVITTTTSCAGCPSMKVLPVLP 72

77 PAVVGNRYDFEFESIRLPGCPRGVNPVSYAVALSCOCALCRSTDCGPKDHLPTCD 136
 73 PQRVCTHRELFASVRLPGCPGVDPVSPVVALSCHRCPLRSLSTDCGGRPRQPLACDH 132

137 PRFOD 141
 133 PPLPD 137

RESULT 10
 LSHB_RAT STANDARD; PRT; 141 AA.

21-JUL-1986 (Rel. 01, Created)
 21-JUL-1986 (Rel. 01, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-beta) (LSH-B) (LH-B).

Rattus norvegicus (Rat).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;

SEQUENCE FROM N.A.
 STRAIN-Sprague-Dawley;
 MEDLINE=83273673; PubMed=6192440;
 Chin W.W., Godine J.E., Klein D.R., Chang A.S., Tan L.K.,
 Habener J.F.;
 "Nucleotide sequence of the cDNA encoding the precursor of the beta subunit of rat lutropin."
 Proc. Natl. Acad. Sci. U.S.A. 80:4649-4653(1983).

SEQUENCE FROM N.A.
 MEDLINE=85080043; PubMed=6096374;
 Jameson L., Chin W.W., Hollenberg A.N., Chang A.S., Habener J.F.;
 "The gene encoding the beta-subunit of rat luteinizing hormone. Analysis of gene structure and evolution of nucleotide sequence."
 J. Biol. Chem. 259:15474-15480(1984).

SEQUENCE OF 4-141 FROM N.A.
 STRAIN-Mistar Imamichi; TISSUE-Anterior pituitary;
 Kato Y., Ezashi T., Hirai T., Kato T.;
 "Strain difference in nucleotide sequences of rat glycoprotein hormone subunit cDNAs and gene fragment."
 Zool. Sci. 7:877-885(1990)

FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.

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EMBL: V01542; CAA24783.1;
 EMBL: J00749; AAN96703.1;
 EMBL: D00576; BAA00454.1;

PIR; A01498; UTRTB.
 PIR; S42527; S42527.
 HSP; P01233; 1XUL.
 InterPro: IPR000359; Cys_knot.
 InterPro: IPR002400; GF_cysknot.
 InterPro: IPR001545; Gly_hormoneb.
 Pfam: PF00007; Cys_knot; 1.
 PRINTS: PR00438; GFCYSKNOT.
 SMART: SM00068; GHB; 1.
 PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
 PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
 Hormone, Signal, Glycoprotein.
 SIGNAL 1 20
 CHAIN 1 141
 DISULFID 29 77
 DISULFID 43 92
 DISULFID 46 130
 DISULFID 54 108
 DISULFID 58 110
 DISULFID 113 120
 CARBOHYD 33 33
 N-LINKED (GLCNAC...) (PROBABLE).

Query Match 44.18; Score 434; DB 1; Length 141;
 Best Local Similarity 62.0%; Pred. No. 6.7e-30;
 Matches 75; Conservative 16; Mismatches 24; Indels 6; Gaps 1;

17 WENGRCDLKEPRPCRPINATLAVEKEGCPVITNTTCAGCPTMRVLOGVLPAL 76
 19 WASRG-----PLRPLCPINATLAEKEKCPVITTTTSCAGCPSMKVLPVLP 72

77 PAVVGNRYDFEFESIRLPGCPRGVNPVSYAVALSCOCALCRSTDCGPKDHLPTCD 136
 73 PQRVCTHRELFASVRLPGCPGVDPVSPVVALSCHRCPLRSLSTDCGGRPRQPLACDH 132

137 P 137
 133 P 133

RESULT 11
 LSHB_CERSI STANDARD; PRT; 141 AA.

077835; O19102;
 16-OCT-2001 (Rel. 40, Created)
 16-OCT-2001 (Rel. 40, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-beta) (LSH-B) (LH-B).

Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
 NCBI_TaxID=9807;

SEQUENCE FROM N.A.
 MEDLINE=98389253; PubMed=9723860;
 Lund L.A., Sherman G.B.;
 "Duplication of the southern white rhinoceros (Ceratotherium simum) lutropin luteinizing hormone beta subunit gene."
 J. Mol. Endocrinol. 21:19-30(1998).

SEQUENCE OF 7-141 FROM N.A.
 TISSUE-Pituitary;
 MEDLINE=97449288; PubMed=9305757;
 Sherman G.B., Lund L.A., Bunick D., Winn R.J.;
 "Characterization and phylogenetic significance of rhinoceros lutropinizing hormone beta (Lhb) subunit messenger RNA structure, complementary DNA sequence and gene copy number."
 Gene 195:131-139(1997).

FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA


```

CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF024521; AAC36049.1; -
CC EMBL; AF024520; AAC36048.1; -
CC EMBL; U72659; AAB71983.1; -
CC HSSP; P01233; 1XUL.
CC InterPro: IPR000359; Cys_knot.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR001545; Gly_hormoneb.
CC Pfam: PF00007; Cys_knot; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC SMART; SM00068; GHb; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC Hormone; Signal; Glycoprotein.
CC CHAIN 1 20 BY SIMILARITY.
CC LUTROPIN BETA CHAIN.
CC FT DISULFID 21 141 BY SIMILARITY.
CC FT DISULFID 29 77 BY SIMILARITY.
CC FT DISULFID 43 92 BY SIMILARITY.
CC FT DISULFID 46 130 BY SIMILARITY.
CC FT DISULFID 54 108 BY SIMILARITY.
CC FT DISULFID 58 110 BY SIMILARITY.
CC FT DISULFID 113 120 BY SIMILARITY.
CC FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 22 22 R -> K (IN REF. 2).
CC SEQUENCE 141 AA; 14930 MW; FFDDB157C51976C9 CRC64;

Query Match 43.5%; Score 428; DB 1; Length 141;
Best Local Similarity 62.8%; Pred. No. 2,1e-29;
Matches 76; Conservative 12; Mismatches 27; Indels 6; Gaps 1;

QY 17 WENPGCRDLKEPLRRCRPNATLAVERKGCVCITVNTTICAGYCPMTRVLYOGVLPAL 76
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 19 WASRG-----PLRPLCRPINATLAENACAPVCITFTTISICAGYCSMVRVLPALPVA 72

QY 77 PQVVCNRYDVRFSIRLPCCPRGNPVVSYAVALSOCALCRSTTDCGPKDHPPLTCD 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 73 PQVVCYHRLRASIIRLPGCPGVDPVMSFVALSCRCGCRLLSSDCGPRAPLACDR 132

QY 137 P 137
DB 133 P 133

RESULT 12
LSHB_PIG STANDARD; PRT; 141 AA.
AC P01232;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91063934; PubMed=1701088;
Ezashi T., Hirai T., Kato T., Wakabayashi K., Kato Y.;

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RT "The gene for the beta subunit of porcine LH: clusters of GC boxes
RT and CACC elements.";
RL J. Mol. Endocrinol. 5:137-146(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89306142; PubMed=2744222;
RA Kato Y., Hirai T.;
RT "Cloning and DNA sequence analysis of the cDNA for the precursor of
RT porcine luteinizing hormone (LH) beta subunit.";
RL Mol. Cell. Endocrinol. 62:47-53(1989).
RN [3]
RP SEQUENCE OF 21-139.
RX MEDLINE=74075724; PubMed=4770795;
RA Maguinn-Rogister G., Hennen G.;
RT "Luteinizing hormone. The primary structures of the beta-subunit from
RT bovine and porcine species.";
RL Eur. J. Biochem. 39:235-253(1973).
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; D00579; BAA00457.1; -
CC PIR; A30322; UTPGB.
CC PIR; A48170; A48170.
CC HSSP; P01233; 1XUL.
CC InterPro: IPR000359; Cys_knot.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR001545; Gly_hormoneb.
CC Pfam: PF00007; Cys_knot; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC SMART; SM00068; GHb; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC Hormone; Signal; Glycoprotein.
CC CHAIN 1 20 LUTROPIN BETA CHAIN.
CC FT DISULFID 21 141 BY SIMILARITY.
CC FT DISULFID 29 77 BY SIMILARITY.
CC FT DISULFID 43 92 BY SIMILARITY.
CC FT DISULFID 46 130 BY SIMILARITY.
CC FT DISULFID 54 108 BY SIMILARITY.
CC FT DISULFID 58 110 BY SIMILARITY.
CC FT DISULFID 113 120 BY SIMILARITY.
CC FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).
CC FT MOD_RES 21 21 BLOCKED.
CC FT VARIANT 30 30 R -> Z.
CC FT CONFLICT 40 40 N -> D (IN REF. 3).
CC FT CONFLICT 62 62 V -> R (IN REF. 3).
CC FT CONFLICT 83 83 S -> I (IN REF. 3).
CC FT CONFLICT 87 87 I -> S (IN REF. 3).
CC FT CONFLICT 122 123 GP -> PG (IN REF. 3).
CC SEQUENCE 141 AA; 14889 MW; 803B8E7C59F3C2CF CRC64;

Query Match 43.4%; Score 427; DB 1; Length 141;
Best Local Similarity 62.8%; Pred. No. 2,6e-29;
Matches 76; Conservative 11; Mismatches 28; Indels 6; Gaps 1;

QY 17 WENPGCRDLKEPLRRCRPNATLAVERKGCVCITVNTTICAGYCPMTRVLYOGVLPAL 76
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 19 WASRG-----PLRPLCRPINATLAENACAPVCITFTTISICAGYCSMVRVLPALPV 72

QY 77 PQVVCNRYDVRFSIRLPCCPRGNPVVSYAVALSOCALCRSTTDCGPKDHPPLTCD 136

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DB 73 PPOVCTYRRLSASTIRLRCPCPGVDPMVSPVALSCHGCRSLSSDCCGPPRAQPLACDR 132
 QY 137 P 137
 DB 133 P 133

RESULT 13
 LSHB_SHEEP STANDARD: PRT; 141 AA.
 ID LSHB_SHEEP STANDARD: PRT; 141 AA.
 AC P01231;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-beta) (LSH-B) (LH-B) (interstitial cell stimulating hormone).
 GN LHB.
 OS Ovis aries (sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprine; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93351742; PubMed=8349025;
 RA Brown P., McNeilly J.R., Wallace R.M., McNeilly A.S., Clark A.J.;
 RT "Characterization of the ovine LH beta-subunit gene: the promoter directs gonadotrope-specific expression in transgenic mice.";
 RL Mol. Cell. Endocrinol. 93:157-165(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93351742; PubMed=8349025;
 RA Brown P., McNeilly J.R., Wallace R.M., McNeilly A.S., Clark A.J.;
 RT "Characterization of the ovine LH beta-subunit gene: the promoter directs gonadotrope-specific expression in transgenic mice.";
 RL Mol. Cell. Endocrinol. 93:157-165(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245669; PubMed=2336396;
 RA D'Angelo-Bernard G., Mounni M., Jutisz M., Counis R.;
 RT "Cloning and sequence analysis of the cDNA for the precursor of the beta subunit of ovine luteinizing hormone.";
 RL Nucleic Acids Res. 18:2175-2175(1990).
 RN [4]
 RP SEQUENCE OF 21-139.
 RX MEDLINE=7221145; PubMed=4556309;
 RA Liu W.-K., Nahm H.S., Sweeney C.M., Holcomb G.N., Ward D.N.;
 RT "The primary structure of ovine luteinizing hormone. II. The amino acid sequence of the reduced, S-carboxymethylated A-subunit (LH-beta).";
 RL J. Biol. Chem. 247:4365-4381(1972).
 RN [5]
 RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
 RX MEDLINE=76068152; PubMed=1201911;
 RA Chung D., Sairam M.R., Li C.H.;
 RT "The primary structure of ovine interstitial cell stimulating hormone. IV. Disulfide bridges of the beta subunit.";
 RL Int. J. Pept. Protein Res. 7:487-493(1975).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE.
 RX MEDLINE=9106170; PubMed=2209620;
 RA Weisshaar G., Hiyama J., Renwick A.G.C.;
 RT "Site-specific N-glycosylation of ovine lutropin. Structural analysis by one- and two-dimensional 1H-NMR spectroscopy.";
 RL Eur. J. Biochem. 192:741-751(1990).
 CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLITROPIN AND GONADOTROPIN.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN

CC FAMILY.
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 CC -----
 DR EMBL; S64695; AAB27819.1; -;
 DR EMBL; X52488; CA36729.1; -;
 DR PIR; A01500; UTSMB.
 DR PIR; S09232; S09232.
 DR HSSP; P01233; 1XUL.
 DR GlycoSuiteDB: P01231; -;
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR002400; GF_cys_knot.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR Pfam: PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GF_CYSKNOT.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 141 LUTROPIN BETA CHAIN.
 FT DISULFID 29 77 BY SIMILARITY.
 FT DISULFID 43 92 BY SIMILARITY.
 FT DISULFID 46 130 BY SIMILARITY.
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120 BY SIMILARITY.
 FT MOD_RES 21 21
 FT CARBOHYD 33 33
 FT VARIANT 138 141 N-LINKED (GLCNAC. . .).
 FT CONFLICT 30 30 /FTID=CAR_000046.
 FT CONFLICT 59 59 MISSING (IN SOME MOLECULES).
 FT CONFLICT 63 63 Q -> E (IN REF. 4).
 FT CONFLICT 71 71 L -> P (IN REF. 1).
 FT CONFLICT 71 71 R -> Q (IN REF. 2).
 FT CONFLICT 81 81 P -> Pp (IN REF. 4).
 FT CONFLICT 81 81 E -> Q (IN REF. 4).
 FT CONFLICT 122 123 GP -> PG (IN REF. 3 AND 4).
 FT CONFLICT 126 126 Q -> E (IN REF. 3 AND 4).
 SQ SEQUENCE 141 AA; 15184 MW; C59EC7C0AA55A9DC CRC44;
 Query Match 43.48; Score 427; DB 1; Length 141;
 Best Local Similarity 60.88; Pred. No. 2; Gaps 1;
 Matches 76; Conservative 14; Mismatches 29; Indels 6; Gaps 1;
 QY 17 WENFGCDLKEPLRRCRPI NATLAVEREGGCPVCITVNTTICAGYCPMTRVLYGVLPAL 76
 DB 19 WASGQ-----PLRPLDOPINATIAAEKACPVCTTTTSCAGYCLSMKRVLPVILPPM 72
 QY 77 PPOVCTYRRLSASTIRLRCPCPGVDPMVSPVALSCHGCRSLSSDCCGPPRAQPLACDR 132
 DB 73 PPOVCTYRRLSASTIRLRCPCPGVDPMVSPVALSCHGCRSLSSDCCGPPRAQPLACDR 132
 QY 137 PPROD 141
 DB 133 PPLPD 137

RESULT 14
 LSHB_MOUSE STANDARD: PRT; 141 AA.
 ID LSHB_MOUSE STANDARD: PRT; 141 AA.
 AC O09108; Q60844;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-beta) (LSH-B) (LH-B).
 GN LHB.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=96125216; PubMed=8543188;
RA Kumar T.R., Matzuk M.M.;
RT "Cloning of the mouse gonadotropin beta-subunit-encoding genes. II.
RT Structure of the luteinizing hormone beta-subunit-encoding genes.";
RL Gene 166:335-336(1995).
RN
RP SEQUENCE OF 18-122 FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=anterior pituitary;
RX Brown P., Brooks J., McNeilly J.R., McNeilly A.S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
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CC -----
DR EMBL: U25145; AAA92841.1;
DR EMBL: Y10418; CAA71445.1;
DR HSSP: P01233; 1XUL.
DR MGD: MGI:96782; lhb.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR001545; Gly_hormoneb.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHb; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KM Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 1 141 BY SIMILARITY.
FT DISULFID 29 77 LUTROPIN BETA CHAIN.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 83 83 A -> R (IN REF. 2).
SQ SEQUENCE 141 AA; 15028 MW; 5E997CABF3D90BF CRC64;

Query Match 43.0%; Score 423; DB 1; Length 141;
Best Local Similarity 60.3%; Pred. No. 5,6e-29;
Matches 73; Conservative 16; Mismatches 26; Indels 6; Gaps 1;

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LSHB_CANFA
ID LSHB_CANFA STANDARD; PRT; 138 AA.
AC P18842;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutein beta chain precursor (luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B) (Fragment).
GN LHB.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88096605; PubMed=3697104;
RT Wolf D.L., Appleby V.L., Hjerild K., Baker A.R., Talmadge K.;
RT "Nucleic acid and amino acid sequences of dog beta LH: comparison to
RT rat, cow and human beta LH.";
RL Nucleic Acids Res. 15:10602-10602(1987).
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
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CC -----
DR EMBL: Y00518; CAA68572.1;
DR PIR: S00512; S00512.
DR HSSP: P01233; 1XUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR001545; Gly_hormoneb.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHb; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KM Hormone; Signal; Glycoprotein.
FT SIGNAL 1 17
FT CHAIN 1 138
FT DISULFID 26 74 BY SIMILARITY.
FT DISULFID 40 89 BY SIMILARITY.
FT DISULFID 43 127 BY SIMILARITY.
FT DISULFID 51 105 BY SIMILARITY.
FT DISULFID 55 107 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 138 AA; 14594 MW; E3639FE6B03F1948 CRC64;

Query Match 42.7%; Score 420; DB 1; Length 138;
Best Local Similarity 62.0%; Pred. No. 9,7e-29;
Matches 75; Conservative 11; Mismatches 29; Indels 6; Gaps 1;

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Thu Nov 21 06:11:39 2002

us-09-787-494-2.rsp

Page 12

Search completed: November 20, 2002, 17:27:58
Job time : 7.01399 secs

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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 21.8671 Seconds

(without alignments)
1667.815 Million cell updates/sec

Title: us-09-787-494-2

Perfect score: 984

Sequence: 1 MTMITTSALAVLORRMENP.....LPSPDPPIPLPOTSHHHHH 177

Scoring table: BLOSUM62

Searched: Gap0 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mmc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	788	80.1	159	4	OBWTT5
2	783	79.6	159	4	OBWXL2
3	776	78.9	159	4	OBWXL3
4	764	77.6	159	4	OBWXL4
5	758	77.0	159	4	OBWXL1
6	738	75.0	157	6	OBWNC5
7	737	74.9	157	6	OBWNC4
8	735	74.7	157	6	OBWNC7
9	726	73.8	157	6	OBWNC6
10	657	66.8	165	6	OBWNC6
11	654	66.5	159	6	OBWNC6
12	653	66.4	159	6	OBWNC6
13	652	66.3	155	6	OBWNC6
14	646	65.7	159	6	OBWNC6
15	646	65.7	159	6	OBWNC6
16	644	65.4	159	6	OBWNC6

17	642	65.2	165	6	O9GL37	O9GL37 macaca mula
18	642	65.2	165	11	O99P48	O99P48 mus musculus
19	631	64.1	159	6	OBWNB3	OBWNB3 colobus gue
20	628	63.8	159	6	OBWNB4	OBWNB4 colobus gue
21	616	62.6	157	6	OBWNB9	OBWNB9 presbytis o
22	615	62.5	157	6	OBWNC3	OBWNC3 presbytis o
23	609	61.9	157	6	OBWNC0	OBWNC0 presbytis o
24	608.5	61.8	157	6	OBWNC1	OBWNC1 presbytis o
25	605	61.5	157	6	OBWNC2	OBWNC2 presbytis o
26	574	58.3	136	6	OBWNB8	OBWNB8 pongo pygma
27	540	54.9	136	4	OBWXL0	OBWXL0 homo sapien
28	515	52.3	136	6	OBWNB6	OBWNB6 presbytis o
29	505	51.3	136	6	OBWNB5	OBWNB5 colobus gue
30	498.5	50.7	156	6	OBWNB6	OBWNB6 aotus triyi
31	498	50.6	136	6	OBWNB7	OBWNB7 macaca mula
32	476.5	48.4	156	6	OBWNA7	OBWNA7 calliobus
33	446	45.3	142	6	O9BD19	O9BD19 panthera tl
34	441	44.8	136	6	OBWNA5	OBWNA5 tarsius ban
35	439	44.6	136	6	OBWNA2	OBWNA2 galago sena
36	437	44.4	136	6	OBWNA4	OBWNA4 daubentonla
37	434	44.1	136	6	OBWNA3	OBWNA3 lemur varie
38	433	44.0	139	11	O62778	O62778 rattus norv
39	431	43.8	136	6	OBWNA0	OBWNA0 cynocephalu
40	430	43.7	136	6	OBWNA1	OBWNA1 loritis tardi
41	429	43.6	136	6	OBWNA1	OBWNA1 pteropus ly
42	413	42.0	136	6	OBWNA9	OBWNA9 cavia porce
43	398	40.4	135	11	O924A7	O924A7 cavia porce
44	398	40.4	141	11	O924A8	O924A8 cavia porce
45	398	40.4	141	11	O924A8	O924A8 cavia porce

ALIGNMENTS

RESULT 1

OBWTT5 PRELIMINARY; PRT; 159 AA.

AC 08WTT5; 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE Choriionic gonadotropin beta subunit (fragment).

GN CGB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Maston G.A., Ruvoilo M.;

RT "Choriionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";

RT Submitted (Jun-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF397577; AAL69705.1; -;

DR EMBL: AF397580; AAL69708.1; -;

DR InterPro: IPR000359; Cys_knot.

DR InterPro: IPR001545; Gly_hormoneB.

DR Pfam: PF00007; Cys_knot; 1.

DR SMART: SM00068; GHB; 1.

DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.

DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.

FT NON_TER 1 1

FT NON_TER 159 159

SO SEQUENCE 159 AA; 16944 MW; 246BA938796A1727 CRC64;

Query Match 80.1%; Score 788; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.7e-74;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 26 KEPLRRRCRPRINATLAVKRGCPVCTVNTTICAGYCPPTWRLGVLPALPOVNCYRD 85
|||||
Db 17 KEPLRRRCRPRINATLAVKRGCPVCTVNTTICAGYCPPTWRLGVLPALPOVNCYRD 76

QY 86 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 145
 Db 77 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 136
 QY 146 KAPPSLPSPSRLLPGSPDPIILP 168
 Db 137 KAPPSLPSPSRLLPGSPDPIILP 159

RESULT 2

Q8WXL2 PRELIMINARY; PRT: 159 AA.
 AC Q8WXL2: 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Choriionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;

QY 26 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 85
 Db 17 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 76
 QY 86 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 145
 Db 77 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 136
 QY 146 KAPPSLPSPSRLLPGSPDPIILP 168
 Db 137 KAPPSLPSPSRLLPGSPDPIILP 159

Query Match 79.6%; Score 783; DB 4; Length 159;
 Best Local Similarity 99.3%; Pred. No. 5.8e-74;
 Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 85
 Db 17 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 76
 QY 86 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 145
 Db 77 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 136
 QY 146 KAPPSLPSPSRLLPGSPDPIILP 168
 Db 137 KAPPSLPSPSRLLPGSPDPIILP 159

QY 26 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 85
 Db 17 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 76
 QY 86 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 145
 Db 77 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 136
 QY 146 KAPPSLPSPSRLLPGSPDPIILP 168
 Db 137 KAPPSLPSPSRLLPGSPDPIILP 159

RESULT 3
 Q8WXL3 PRELIMINARY; PRT: 159 AA.
 AC Q8WXL3: 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Choriionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;

QY 26 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 85
 Db 17 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 76
 QY 86 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 145
 Db 77 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 136
 QY 146 KAPPSLPSPSRLLPGSPDPIILP 168
 Db 137 KAPPSLPSPSRLLPGSPDPIILP 159

RT evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF397578; AAL69706.1; -
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR001545; Gly_hormoneb.
 DR Pfam: PF00007; Cys_knot; 1.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 17006 MW; AFDCACE2542BC084 CRC64;

Query Match 78.9%; Score 776; DB 4; Length 159;
 Best Local Similarity 98.6%; Pred. No. 3.1e-73;
 Matches 141; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 26 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 85
 Db 17 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 76
 QY 86 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 145
 Db 77 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 136
 QY 146 KAPPSLPSPSRLLPGSPDPIILP 168
 Db 137 KAPPSLPSPSRLLPGSPDPIILP 159

RESULT 4

Q8WXL4 PRELIMINARY; PRT: 159 AA.
 AC Q8WXL4: 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Choriionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;

QY 26 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 85
 Db 17 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 76
 QY 86 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 145
 Db 77 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 136
 QY 146 KAPPSLPSPSRLLPGSPDPIILP 168

Query Match 77.6%; Score 764; DB 4; Length 159;
 Best Local Similarity 97.2%; Pred. No. 5.6e-72;
 Matches 139; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 26 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 85
 Db 17 KEPLRPRCPINATLAVEKESCPVCTVNTTICAGYCPRTVRLQGVLPALPOVVCNYRD 76
 QY 86 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 145
 Db 77 VRFESIRLPGCPGCVNPNVSYAVALSCQCALCRSTTDCGGPKDHPJLTCDDPRFQDSSS 136
 QY 146 KAPPSLPSPSRLLPGSPDPIILP 168

ID	ORGANISM	PRELIMINARY	PRT	159 AA
DB	137 KAPPSLPSPSRLPGSPDPIPLP	159		
RESULT 5				
ID	08WXL1	PRELIMINARY	PRT	159 AA
AC	08WXL1			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Chorionic gonadotropin beta subunit (Fragment).			
GN	CGA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Maston G.A., Ruvolo M.;			
RT	"Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";			
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF397381; AAL69709.1; -			
DR	InterPro; IPR000359; Cys_knot.			
DR	InterPro; IPR001545; Gly_hormoneB.			
DR	Pfam; PF00007; Cys_knot; 1.			
DR	SMART; SM00068; GHB; 1.			
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.			
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.			
FT	NON_TER 1			
FT	NON_TER 159			
SO	SEQUENCE 159 AA; 16969 MW; 3C963B3C3D2E57FE CRC64;			
Query Match 77.0%; Score 758; DB 4; Length 159;				
Best local similarity 96.5%; Pred. No. 2.4e-71;				
Matches 138; Conservative 1; Mismatches 4; Indels 0; Gaps 0				
QY	26 KEPLRRCPRINATLAVEKEGCPVCITVNTTICAGYCPMTREVLGVLPALPQVCNRYD	85		
DB	17 REPLRPWCHPINALIAREGCPVCITVNTTICAGYCPMTREVLGVLPALPQVCNRYD	76		
QY	86 VFEESIRLPGCGRGVNPVSVAVALSQCALCRSTDCGGRKHDLTCDPDRFDQSSSS	145		
DB	77 VFEESIRLPGCGRGVNPVSVAVALSQCALCRSTDCGGRKHDLTCDPDRFDQSSSS	136		
QY	146 KAPPSLPSPSRLPGSPDPIPLP	168		
DB	137 KAPPSLPSPSRLPGSPDPIPLP	159		
RESULT 6				
ID	08WNC5	PRELIMINARY	PRT	157 AA
AC	08WNC5			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Chorionic gonadotropin beta subunit (Fragment).			
GN	CGA.			
OS	Pongo pygmaeus (Orangutan).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.			
OX	NCBI_TaxID=9600;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Maston G.A., Ruvolo M.;			
RT	"Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";			
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF397584; AAL69712.1; -			
DR	InterPro; IPR000359; Cys_knot.			
DR	InterPro; IPR001545; Gly_hormoneB.			

	DR	pfam: PF00007; Cys_knot; 1.
	DR	SMART: SMO0068; GHb; 1.
	DR	PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
	DR	PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
	FT	NON_TER 1
	FT	NON_TER 1
SQ	SEQUENCE	157 AA; 17027 MW; 8317774E0F4BD4ED CRC64;
	Query Match	75.0%; Score 738; DB 6; Length 157;
	Best Local Similarity	86.1%; Pred. No. 2.8e-69;
	Matches 136; Conservative	4; Mismatches 12; Indels 6; Gaps 1;
OY	8	LAVVILRQRWMEPCGRDLEKEPLRPICRIPIATLAIEKEGCPVCITVTNTTICAGYCPTMT 67
	I : :	
DB	5	LMLSMGRWAS-----KEPLRPICRIPIATLAIEKEGCPVCIVTNTTICAGYCPTMR 58
OY	68	VLAGVLPAIPQVVNCNRDVREFSIRLPGCGRCGVNPNVSVAVALSCQCALCRSTTDGCGP 127
	I : :	
DB	59	VLAGVLPRLPQVVCNVRDVFREYIRLPGCGRCGVNPNVSVAVALSCQCALCRSTTDGCGP 118
OY	128	KDHPLTCDDPRFDSSSKAPPPSLPSRLGPSPDT 165
	I : :	
DB	119	KDHPLTCDDPRFDPPSSSKAPPPSLPSRLPEPSTDTP 156
	RESULT 7	
	ID OBNMC4	PRELIMITARY; PRT: 157 AA.
AC	OBNMC4:	
DT	01-MAR-2002 (TREMBLrel. 20, Created)	
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	Chorionic gonadotropin beta subunit (Fragment).	
GN	CGB.	
OS	Pongo pygmaeus (Orangutan).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.	
NCBI_TaxID=9600;		
RN	(1)	
RP	SEQUENCE FROM N.A.	
RA	Maston G.A., Ruvolo M.;	
RT	"Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection";	
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
RL	EMBL; AF397585; AAL69713.1; -	
DR	InterPro: IPR000359; Cys_knot.	
DR	InterPro: IPR001545; Gly_hormoneb.	
DR	pfam: PF00007; Cys_knot; 1.	
DR	SMART: SMO0068; GHb; 1.	
DR	PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.	
DR	PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.	
FT	NON_TER 1	
FT	NON_TER 1	
SQ	SEQUENCE	157 AA; 157 MW; 825D27AC3EFBD4F6 CRC64;
	Query Match	74.9%; Score 737; DB 6; Length 157;
	Best Local Similarity	93.0%; Pred. No. 3.6e-69;
	Matches 133; Conservative	2; Mismatches 5; Indels 0; Gaps 0;
OY	26	KEPLLPRCIPINATIAVEKGCPCVITVTNTTICAGYCPTMTVLGGVLPALPOVCNVRD 85
	I : :	
DB	17	KEPLRPICRIPIATLAIEKEGCPVCIVTNTTICAGYCPTMTVLSYLPLPQQVCNVRD 76
OY	86	VAFESIRLFGCGRVNPVSVAYVALSCQCALCRSTTDGCGKHPLTCDDPRFDSSSS 145
	I : :	
DB	77	VAFEXIRLPGCGRVNPNVSVAVALSCQCALCRSTTDGCGKHPLTCDDPRFDPSSS 136
OY	146	KAPPSPSLPSRLGPSPT 165
	I : :	
DB	137	KAPPSPSLPSRLPEPSTNP 156
	RESULT 8	

```
08MNC7
ID 08MNC7 PRELIMINARY: PRT: 157 AA.
AC 08MNC7:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Choriionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvoio M.;
RT "Choriionic gonadotropin has a recent origin in primates and an
RT evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF397582; AAL69710.1; -.
DR InterPro: IPR000359; Cys_knot.
DR Pfam: PF00007; Cys_knot.1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 157 AA; 16928 MW; 825D27A00EFBD46 CRC64;

Query Match
Best Local Similarity 74.7%; Score 735; DB 6; Length 157;
Matches 133; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 26 KEPLRRCRPNATLAVEKEGCPVCITVNTTICAGYCPMTRVLGVLPAALPOVVCNRYD 85
Db 17 KEPLRRCRPNATLAVEKEGCPVCITVNTTICAGYCPMTRVLGVLPAALPOVVCNRYD 76
Qy 86 VFESIRLPGCGRGVNPVSYAVALSOCALCRSTTCGGPKHPLTCDDPRDDSSS 145
Db 77 VFESIRLPGCGRGVNPVSYAVALSOCALCRSTTCGGPKHPLTCDDPRDDPS 136
Qy 146 KAPPSLPSPSLRPGSDTP 165
Db 137 KAPPSLPSPSLRPGSDTP 156

RESULT 9
08MNC6
ID 08MNC6 PRELIMINARY: PRT: 157 AA.
AC 08MNC6:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Choriionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvoio M.;
RT "Choriionic gonadotropin has a recent origin in primates and an
RT evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF397583; AAL69711.1; -.
DR InterPro: IPR000359; Cys_knot.
DR Pfam: PF00007; Gly_hormoneb.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 1
```

```
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 16868 MW; 97BD27A014E1D4EC CRC64;

Query Match
Best Local Similarity 73.8%; Score 726; DB 6; Length 157;
Matches 132; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 26 KEPLRRCRPNATLAVEKEGCPVCITVNTTICAGYCPMTRVLGVLPAALPOVVCNRYD 85
Db 17 KEPLRRCRPNATLAVEKEGCPVCITVNTTICAGYCPMTRVLGVLPAALPOVVCNRYD 76
Qy 86 VFESIRLPGCGRGVNPVSYAVALSOCALCRSTTCGGPKHPLTCDDPRDDSSS 145
Db 77 VFESIRLPGCGRGVNPVSYAVALSOCALCRSTTCGGPKHPLTCDDPRDDPS 136
Qy 146 KAPPSLPSPSLRPGSDTP 165
Db 137 KAPPSLPSPSLRPGSDTP 156

RESULT 10
09BEH1
ID 09BEH1 PRELIMINARY: PRT: 165 AA.
AC 09BEH1:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Choriionic gonadotropin beta subunit 2.
OS Macaca fascicularis (Crah eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
RT "A Comparison of Choriionic gonadotropin Expression by Human and
RT Macaque Trophoblast Cells.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY026360; AAK08644.1; -.
DR HSSP: P01233; IXUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR001545; Gly_hormoneb.
DR Pfam: PF00007; Gly_knot.1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ SEQUENCE 165 AA; 17743 MW; 2F21566B48592471 CRC64;

Query Match
Best Local Similarity 66.8%; Score 657; DB 6; Length 165;
Matches 120; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Qy 21 GCRDLKRLRRCRPNATLAVEKEGCPVCITVNTTICAGYCPMTRVLGVLPAALPOV 80
Db 17 GARASREPLRLCRPNATLAVEKEACPCITVNTTICAGYCPMTRVLGVLPAALPOV 76
Qy 81 CNYRDVFESIRLPGCGRGVNPVSYAVALSOCALCRSTTCGGPKHPLTCDDPRFQ 140
Db 77 CNYRDVFESIRLPGCGRGVNPVSYAVALSOCALCRSTTCGGPKHPLTCDDPRFQ 136
Qy 141 DSSSKAPPSLPSPSLRPGSDTPILQ 169
Db 137 ASSSSKPPSPSPSLRPGSDTPILQ 165

RESULT 11
08MNB0
ID 08MNB0 PRELIMINARY: PRT: 159 AA.
AC 08MNB0:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
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DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Choriionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
NCBI_TaxID=9544;
OX
RN
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvoilo M.;
RT "Choriionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF397600; AAL69728.1; -
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneb.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 159
SQ SEQUENCE 159 AA; 16915 MW; 7864051C2P863870 CRC64;

Query Match 66.5%; Score 654; DB 6; Length 159;
Best Local Similarity 81.1%; Pred. No. 1.7e-60;
Matches 120; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 21 GCRDLKEPLRPGRPIINATLAVERGCPVITYNTTICAGCPTMTRVLOGVLPALPOV 80
DB 12 GARASREPLRLPCRPINATLAERKACPCIVNTTICAGCPTMTRVLOGVLPALPOV 71
QY 81 CNRYDVFESIRLPGCPGVNPNVSYAVALSQCACALCRSTDCGPKDHPITCDDPRFQ 140
DB 72 CNRYREVRESIRLPGCPGVDPVSVVVALSCRCALCRSTDCGPKDHPITCDDPHLQ 131
QY 141 DSSSKAPPSLPSRLPGSDPTPLP 168
DB 132 ASSSKDPPSPSPSLLEPADTPEFLP 159

RESULT 12
Q8WNB2 PRELIMINARY; PRT; 159 AA.
AC Q8WNB2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Choriionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
NCBI_TaxID=9544;
OX
RN
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvoilo M.;
RT "Choriionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF397601; AAL69729.1; -
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneb.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 159
SQ SEQUENCE 159 AA; 16915 MW; 9231691ED0D82863 CRC64;
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Query Match 66.4%; Score 653; DB 6; Length 159;
Best Local Similarity 80.4%; Pred. No. 2.1e-60;
Matches 119; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 21 GCRDLKEPLRPGRPIINATLAVERGCPVITYNTTICAGCPTMTRVLOGVLPALPOV 80
DB 12 GARASREPLRLPCRPINATLAERKACPCIVNTTICAGCPTMTRVLOGVLPALPOV 71
QY 81 CNRYDVFESIRLPGCPGVNPNVSYAVALSQCACALCRSTDCGPKDHPITCDDPRFQ 140
DB 72 CNRYREVRESIRLPGCPGVDPVSVVVALSCRCALCRSTDCGPKDHPITCDDPHLQ 131
QY 141 DSSSKAPPSLPSRLPGSDPTPLP 168
DB 132 ASSSKDPPSPSPSLLEPADTPEFLP 159

RESULT 13
Q9BEH2 PRELIMINARY; PRT; 165 AA.
AC Q9BEH2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Choriionic gonadotropin beta subunit 1.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
NCBI_TaxID=9541;
OX
RN
RP SEQUENCE FROM N.A.
RA TISSUE-EMBRONIC TROPHOBLAST;
RC Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
RT "A comparison of choriionic gonadotropin expression by human and
macaque trophoblast cells.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AV026359; AAK08643.1; -
DR HSSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneb.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ SEQUENCE 165 AA; 17711 MW; 280DF602157D9940 CRC64;

Query Match 66.3%; Score 652; DB 6; Length 165;
Best Local Similarity 79.9%; Pred. No. 2.8e-60;
Matches 119; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 21 GCRDLKEPLRPGRPIINATLAVERGCPVITYNTTICAGCPTMTRVLOGVLPALPOV 80
DB 17 GARASREPLRLPCRPINATLAERKACPCIVNTTICAGCPTMTRVLOGVLPALPOV 76
QY 81 CNRYDVFESIRLPGCPGVNPNVSYAVALSQCACALCRSTDCGPKDHPITCDDPRFQ 140
DB 77 CNRYREVRESIRLPGCPGVDPVSVVVALSCRCALCRSTDCGPKDHPITCDDPHLQ 136
QY 141 DSSSKAPPSLPSRLPGSDPTPLP 169
DB 137 ASSSKDPPSPSPSLLEPADTPEFLP 165

RESULT 14
Q8WNB2 PRELIMINARY; PRT; 159 AA.
AC Q8WNB2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Choriionic gonadotropin beta subunit (Fragment).
GN CGB.
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OY      23  BDLEKLEPPRRPPIATIAVAKEGCPVITYNTTICAGICTPMTRVLOGVLPALPQVVCN  82
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Db      14  RASRLEPRLPLCGPIATIAAEKACPVITYNTTICAGICTPMKRVLOVILIPVQVVCN  73

OY      83  YRDVFEESIRLPGCGRGVNPVYSVAVALSCOCALCRSTYDGGGPKDHPLETCDDPFDOS  147
      | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db      74  YREVFESIRLPGCGPGVDVPSVSVVALSCALCRSTSDCGGPKDHPLETCDDPFDOS  137

OY      143  SSKAPPSLPSPSRLPGSPDPLP  168
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Db      134  SSKDPPSPSPSRLLERADTPLP  159

Search completed: November 20, 2002, 17:28:59
Job time : 22.8671 secs

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Search completed: November 20, 2002, 17:28:59
Job time : 22.8671 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:29:06 ; Search time 5.77622 Seconds
(without alignments)
479.913 Million cell updates/sec

Title: US-09-787-494-2

Perfect score: 984
Sequence: 1 MTMTDSLAVYLQRRDMEP.....LPGPSDTPLPQSHNNHHN 177

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 100480 segs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	80.6	165	9	US-09-915-676-1
2	793	80.6	165	10	US-09-466-320-14
3	767	77.9	307	10	US-09-756-186-4
4	767	77.9	336	10	US-09-756-186-8
5	766	77.8	141	9	US-09-813-398-3
6	611	62.1	195	10	US-09-780-933-30
7	611	62.1	196	10	US-09-780-933-29
8	540	54.9	122	9	US-09-813-398-4
9	437	44.4	141	10	US-09-730-617-47
10	427	43.4	141	10	US-09-730-617-48
11	382	38.8	113	10	US-09-730-617-44
12	371	37.7	99	10	US-09-730-617-41
13	303	30.8	140	10	US-09-730-617-46
14	303	30.8	144	10	US-09-730-617-45
15	265.5	27.0	116	10	US-09-730-617-38
16	265	26.9	85	10	US-09-730-617-35
17	247	25.1	119	9	US-09-813-398-2
18	227	23.1	111	9	US-09-973-918A-4
19	226	23.0	110	9	US-09-813-398-5

20	215	21.8	108	9	US-09-973-918A-11	Sequence 11, Appl
21	215	21.8	109	9	US-09-973-918A-12	Sequence 12, Appl
22	215	21.8	110	9	US-09-973-918A-13	Sequence 13, Appl
23	215	21.8	111	9	US-09-973-918A-6	Sequence 6, Appl
24	215	21.8	111	9	US-09-973-918A-10	Sequence 10, Appl
25	215	21.8	111	10	US-09-780-933-4	Sequence 4, Appl
26	215	21.8	129	10	US-09-780-933-3	Sequence 3, Appl
27	215	21.8	129	10	US-09-780-933-23	Sequence 23, Appl
28	215	21.8	116	9	US-09-780-933-28	Sequence 28, Appl
29	209	21.2	111	9	US-09-973-918A-2	Sequence 2, Appl
30	208	21.1	111	9	US-09-973-918A-8	Sequence 8, Appl
31	204	20.7	38	9	US-09-915-676-3	Sequence 3, Appl
32	204	20.7	38	10	US-09-466-320-2	Sequence 2, Appl
33	204	20.7	65	10	US-09-466-320-12	Sequence 12, Appl
34	204	20.7	66	10	US-09-466-320-13	Sequence 13, Appl
35	204	20.7	68	10	US-09-466-320-11	Sequence 11, Appl
36	202	20.5	37	9	US-09-915-676-1	Sequence 2, Appl
37	202	20.5	37	10	US-09-466-320-1	Sequence 1, Appl
38	143	14.5	106	9	US-09-943-388-9	Sequence 9, Appl
39	143	14.5	106	10	US-09-818-954A-3	Sequence 3, Appl
40	143	14.5	130	9	US-09-943-388-2	Sequence 2, Appl
41	143	14.5	130	9	US-09-943-388-5	Sequence 5, Appl
42	143	14.5	130	10	US-09-818-954A-1	Sequence 1, Appl
43	141	14.3	106	10	US-09-818-954A-13	Sequence 13, Appl
44	141	14.3	130	9	US-09-943-388-23	Sequence 23, Appl
45	141	14.3	130	10	US-09-818-954A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-915-676-1
; Sequence 1, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRP
; ORGANISM: Homo sapiens
; US-09-915-676-1

Query Match 80.6%; Score 793; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-57;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRPRCPINATLAVEKEECPCVITVNTTICAGYCPMTRVLOGVLPALPQVVCNRD 85
DB 22 KEPLRPRCPINATLAVEKEECPCVITVNTTICAGYCPMTRVLOGVLPALPQVVCNRD 81
QY 86 VRESITLPCGPRGVNVVSAVALSCQALCRSTDDCGSPKRNHPLTCDDPRDSSSS 145
DB 82 VRESITLPCGPRGVNVVSAVALSCQALCRSTDDCGSPKRNHPLTCDDPRDSSSS 141
QY 146 KAPPSLPSPSRILPGPSDTPLPQ 169
DB 142 KAPPSLPSPSRILPGPSDTPLPQ 165

RESULT 2
US-09-466-320-14
Sequence 14, Application US/09466320
Patent No. US20020025939A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick
TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
TITLE OF INVENTION: Methods
FILE REFERENCE: 0450-0026.30
CURRENT APPLICATION NUMBER: US/09/466,320
CURRENT FILING DATE: 1999-12-17
EARLIER APPLICATION NUMBER: US 60/112,910
EARLIER FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 165
TYPE: PRP
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hcg beta sub unit
US-09-466-320-14

Query Match
Best Local Similarity 80.6%; Score 793; DB 10; Length 165;
Matches 144; Conservative 0; Pred. No. 1.3e-57;
Mismatch 0; Indels 0; Gaps 0;

QY 26 KEPLRRRCRPI NATLAVEREGCPVCITVNTTICAGYCPMTRVLGVPALPOVVCNYRD 85
DB 22 KEPLRRRCRPI NATLAVEREGCPVCITVNTTICAGYCPMTRVLGVPALPOVVCNYRD 81
QY 86 VFESIRLPGCGRGVNPVSYAVALSQCQALCRSTTDCGGPKDHPPLTCDPRFODSSSS 145
DB 82 VFESIRLPGCGRGVNPVSYAVALSQCQALCRSTTDCGGPKDHPPLTCDPRFODSSSS 141
QY 146 KAPPSLPSPSRPLGPSDTPILPQ 169
DB 142 KAPPSLPSPSRPLGPSDTPILPQ 165

RESULT 3
US-09-756-186-4
Sequence 4, Application US/09756186
Patent No. US20010014333A1
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-756-186-4

Query Match
Best Local Similarity 77.9%; Score 767; DB 10; Length 307;
Matches 139; Conservative 0; Pred. No. 3.2e-55;
Mismatch 0; Indels 0; Gaps 0;

QY 31 PRCRPI NATLAVEREGCPVCITVNTTICAGYCPMTRVLGVPALPOVVCNYRDVRES 90
DB 169 PRCRPI NATLAVEREGCPVCITVNTTICAGYCPMTRVLGVPALPOVVCNYRDVRES 228
QY 91 IRLPGCGRGVNPVSYAVALSQCQALCRSTTDCGGPKDHPPLTCDPRFODSSSKAPP 150
DB 229 IRLPGCGRGVNPVSYAVALSQCQALCRSTTDCGGPKDHPPLTCDPRFODSSSKAPP 288
QY 151 SLSPSRPLGPSDTPILPQ 169
DB 289 SLSPSRPLGPSDTPILPQ 307

RESULT 4
US-09-756-186-8
Sequence 8, Application US/09756186
Patent No. US20010014333A1
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-756-186-8

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Query Match          77.9%; Score 767; DB 10; Length 336;
Best Local Similarity 100.0%; Pred. No. 3,6e-55;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       198 PCRCPINATLAVKEGCGVCITVNTTTCAGCYCPTMTPTVLGVLPALPOVCNTRYDRFES 257
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QY      91  IRLPCGPGVNPVVSAYAVALSOCALCRSTTDCGSPKDHPLTCDPFRFODSSSSKAPP 150
         |||||||
Db       258 IRLPCGPGVNPVVSAYAVALSOCALCRSTTDCGSPKDHPLTCDPFRFODSSSSKAPP 317
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QY      151 SLSPSRLPGSPDPTLPQ 169
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Db       318 SLSPSRLPGSPDPTLPQ 336
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RESULT 5
US-09-813-398-3
: Sequence 3, Application US/09813398
: Patent No. US20020169292A1
: GENERAL INFORMATION:
: APPLICANT: Bruce D. Weintraub
: APPLICANT: Mariusz W. Szkudlinski
: APPLICANT: University of Maryland
: TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
: FILE REFERENCE: UOFMD.003C1
: CURRENT APPLICATION NUMBER: US/09/813.398
: PRIOR FILING DATE: 2001-03-20
: PRIOR APPLICATION NUMBER: PCT/US99/05908
: PRIOR FILING DATE: 1999-03-19
: PRIOR APPLICATION NUMBER: PCT/US98/19772
: PRIOR FILING DATE: 1998-09-22
: NUMBER OF SEQ ID NOS: 41
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 141
: TYPE: PRT
: ORGANISM: HOMO SAPIEN
US-09-813-398-3

Query Match          77.8%; Score 766; DB 9; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.7e-55;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26  KEPLRPCRPIATLAVKEGCGVCITVNTTTCAGCYCPTMTPTVLGVLPALPOVCNRYD 85
         |||||||
Db       3  KEPLRPCRPIATLAVKEGCGVCITVNTTTCAGCYCPTMTPTVLGVLPALPOVCNRYD 62
         |||||||

QY      86  VRFESIRLPGCPGPNPVVSAYAVALSOCALCRSTTDCGSPKDHPLTCDPFRFODSSSS 145
         |||||||
Db       63  VRFESIRLPGCPGPNPVVSAYAVALSOCALCRSTTDCGSPKDHPLTCDPFRFODSSSS 122
         |||||||

QY      146 KAPPSLSPSRLPGPSDT 164
         |||||||
Db       123 KAPPSLSPSRLPGPSDT 141
         |||||||

RESULT 6
US-09-780-933-30
: Sequence 30, Application US/09780933
: Patent No. US20020127652A1
: GENERAL INFORMATION:
: APPLICANT: SCHAMBE, HANS T.
: APPLICANT: ANDERSEN, KIM V.
: APPLICANT: VAN DEN HAZEL, BART
: APPLICANT: CHRISTIANSEN, JESPER
: APPLICANT: JEPPESEN, CLAUD B.
: TITLE OF INVENTION: POLYCLE STIMULATING HORMONES
: FILE REFERENCE: 31-001000US
: CURRENT APPLICATION NUMBER: US/09/780.933
: CURRENT FILING DATE: 2001-02-09

```

```

      1  PRIOR APPLICATION NUMBER: PA 2000 00220
      2  PRIOR FILING DATE: 2000-02-11
      3  PRIOR APPLICATION NUMBER: 60/184, 035
      4  PRIOR FILING DATE: 2000-02-22
      5  PRIOR APPLICATION NUMBER: PA 2000 01092
      6  PRIOR FILING DATE: 2000-07-14
      7  PRIOR APPLICATION NUMBER: 60/225, 558
      8  PRIOR FILING DATE: 2000-08-16
      9  NUMBER OF SEQ ID NOS: 30
     10  SOFTWARE: PatentIn Ver. 2.1
     11  SEQ ID NO 30
     12  LENGTH: 195
     13  TYPE: PRT
     14  ORGANISM: Homo sapiens
     15  US-09-780-933-30
  Query Match
  Best Local Similarity 100.0%; Score 611; DB 10; Length 195;
  Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  26  KEPLRRCRPIATLAVEKEGCPVCITVNTTTCAGYCPMTFVLGVLPALPQVVCNTRD 85
  86  KEPLRRCRPIATLAVEKEGCPVCITVNTTTCAGYCPMTFVLGVLPALPQVVCNTRD 145
  146  VFESIRLPGCRGVNPNVSYAVALSOCALCRSTTDCGGKDHPLTCD 195
  RESULT 7
  US-09-780-933-29
  Sequence 29, Application US/09780933
  Patent No. US20020127652A1
  GENERAL INFORMATION:
  APPLICANT: SCHAMBEY, HANS T.
  APPLICANT: ANDERSEN, KIM V.
  APPLICANT: VAN DEN HAZEL, BART
  APPLICANT: CHRISTIANSEN, JESPER
  APPLICANT: JEPPESEN, CLAUD B.
  TITLE OF INVENTION: POLICICLE STIMULATING HORMONES
  FILE REFERENCE: 31-00100005
  CURRENT APPLICATION NUMBER: US/09/780, 933
  CURRENT FILING DATE: 2001-02-09
  PRIOR APPLICATION NUMBER: PA 2000 00220
  PRIOR FILING DATE: 2000-02-11
  PRIOR APPLICATION NUMBER: 60/184, 035
  PRIOR FILING DATE: 2000-02-22
  PRIOR APPLICATION NUMBER: PA 2000 01092
  PRIOR FILING DATE: 2000-07-14
  PRIOR APPLICATION NUMBER: 60/225, 558
  PRIOR FILING DATE: 2000-08-16
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 29
  LENGTH: 196
  TYPE: PRT
  ORGANISM: Homo sapiens
  US-09-780-933-29
  Query Match
  Best Local Similarity 100.0%; Score 611; DB 10; Length 196;
  Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  26  KEPLRRCRPIATLAVEKEGCPVCITVNTTTCAGYCPMTFVLGVLPALPQVVCNTRD 85
  87  KEPLRRCRPIATLAVEKEGCPVCITVNTTTCAGYCPMTFVLGVLPALPQVVCNTRD 146
  86  VFESIRLPGCRGVNPNVSYAVALSOCALCRSTTDCGGKDHPLTCD 135
  147  VFESIRLPGCRGVNPNVSYAVALSOCALCRSTTDCGGKDHPLTCD 196
  RESULT 8

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US-09-813-398-4
; Sequence 4, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Marusz W. Szudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: USFMD.00301
; CURRENT APPLICATION NUMBER: US/09/813.398
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 122
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-4

Query Match
Best Local Similarity 54.9%; Score 540; DB 9; Length 122;
Matches 96; Conservativity 6; Mismatches 11; Indels 0; Gaps 0;
OY 26 KEPLRPRCPINATLAVERKGCPCVITVNTTTCAGYCPMTTRVLOGVLPALPQVNCNRD 85
Db 3 REPLRPRCPINATLAVERKGCPCVITVNTTTCAGYCPMTTRVLOGVLPALPQVNCNRD 85
OY 86 VRFESIRLRCGPRGVNPNVSYAVALSQCACLRSTTDCGGRKDPHPLTCDDP 138
Db 63 VRFESIRLRCGPRGVNPNVSYAVALSQCACLRSTTDCGGRKDPHPLTCDDP 115

RESULT 9
US-09-730-617-47
; Sequence 47, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Mezes, Peter S
; FILE REFERENCE: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
; CURRENT APPLICATION NUMBER: US/09/730.617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-730-617-47

Query Match
Best Local Similarity 44.4%; Score 437; DB 10; Length 141;
Matches 77; Conservativity 14; Mismatches 28; Indels 6; Gaps 1;

OY 17 WENPCRDLEKPLRRCRPIATLAVERKGCPCVITVNTTTCAGYCPMTTRVLOGVLPAL 76
Db 19 WASRG-----PLRPLCPINATLAVERKGCPCVITVNTTTCAGYCPMTTRVLOGVLPAL 72
OY 77 PQVVCNRYDVRFESIRLRCGPRGVNPNVSYAVALSQCACLRSTTDCGGRKDPHPLTCDD 136
Db 73 PQVVCNRYDVRFESIRLRCGPRGVNPNVSYAVALSQCACLRSTTDCGGRKDPHPLTCDD 136
OY 137 PRFOD 141
Db 133 PRLPD 137

RESULT 10
US-09-730-617-48
; Sequence 48, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Mezes, Peter S
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730.617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-730-617-48

Query Match
Best Local Similarity 43.4%; Score 427; DB 10; Length 141;
Matches 76; Conservativity 14; Mismatches 29; Indels 6; Gaps 1;
OY 17 WENPCRDLEKPLRRCRPIATLAVERKGCPCVITVNTTTCAGYCPMTTRVLOGVLPAL 76
Db 19 WASRG-----PLRPLCPINATLAVERKGCPCVITVNTTTCAGYCPMTTRVLOGVLPAL 72
OY 77 PQVVCNRYDVRFESIRLRCGPRGVNPNVSYAVALSQCACLRSTTDCGGRKDPHPLTCDD 136
Db 73 PQVVCNRYDVRFESIRLRCGPRGVNPNVSYAVALSQCACLRSTTDCGGRKDPHPLTCDD 136
OY 137 PRFOD 141
Db 133 PRLPD 137

RESULT 11
US-09-730-617-44
; Sequence 44, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D

```
;; APPLICANT: Mezes, Peter S
;; TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
;; FILE REFERENCE: 15966-609
;; CURRENT APPLICATION NUMBER: US/09/730,617
;; CURRENT FILING DATE: 2000-12-05
;; PRIOR APPLICATION NUMBER: 60/169,056
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: 60/169,886
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/170,252
;; PRIOR FILING DATE: 1999-12-10
;; PRIOR APPLICATION NUMBER: 60/175,740
;; PRIOR FILING DATE: 2000-01-12
;; NUMBER OF SEQ ID NOS: 100
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 44
;; LENGTH: 113
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-730-617-44
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Query Match          38.8%; Score 382; DB 10; Length 113;
Best Local Similarity 63.6%; Pred. No. 1.4e-24;
Matches 68; Conservative 12; Mismatches 21; Indels 6; Gaps 1;
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OY 17 WENPCRDLCRPLRCRCRINATLAVEKEGCVICITVNTTICAGYCPMTRVLOGVLPAL 76
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DB 13 WASRG-----PLRPLCRINATLAEKACICITFTTISICAGCPSVWRVPALPAI 66
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 77 PQVCNRYRDVRESIRLPGCPRGVNPVSYAVALSOCALCRSTTD 123
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 67 PQVCTYRELRFASIRLPGCPRGVDPVMSFVVALSCHGCPCKRTTD 113
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 12
US-09-730-617-41
;; Sequence 41, Application US/09730617
;; Patent No. US20020068279A1
;; GENERAL INFORMATION:
;; APPLICANT: Burgess, Catherine E
;; APPLICANT: Prayaga, Sudhirdas K
;; APPLICANT: Shinkets, Richard A
;; APPLICANT: Rastelli, Luca
;; APPLICANT: Zerhusen, Bryan D
;; APPLICANT: Mezes, Peter S
;; TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
;; FILE REFERENCE: 15966-609
;; CURRENT APPLICATION NUMBER: US/09/730,617
;; CURRENT FILING DATE: 2000-12-05
;; PRIOR APPLICATION NUMBER: 60/169,056
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: 60/169,886
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/169,866
;; PRIOR FILING DATE: 1999-12-10
;; PRIOR APPLICATION NUMBER: 60/170,252
;; PRIOR FILING DATE: 1999-12-10
;; PRIOR APPLICATION NUMBER: 60/175,740
;; PRIOR FILING DATE: 2000-01-12
;; NUMBER OF SEQ ID NOS: 100
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 41
;; LENGTH: 99
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-730-617-41
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Query Match          37.7%; Score 371; DB 10; Length 99;
Best Local Similarity 67.7%; Pred. No. 9.2e-24;
Matches 65; Conservative 12; Mismatches 19; Indels 0; Gaps 0;
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OY 28 PLRRCRPNATLAVEKEGCVICITVNTTICAGYCPMTRVLOGVLPALPOVCNTRDVR 87
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 4 PLRPLQPIINATLAEKACIPVCITFTTISICAGCPSMKRVLPLVILPMPQRYCTYHEL 63
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 88 FESIRLPGCPRGVNPVSYAVALSOCALCRSTTD 123
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 64 FASVRLPGCPRGVDPVMSFVVALSCHGCPCKRTSSTD 99
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RESULT 13
US-09-730-617-46
;; Sequence 46, Application US/09730617
;; Patent No. US20020068279A1
;; GENERAL INFORMATION:
;; APPLICANT: Burgess, Catherine E
;; APPLICANT: Prayaga, Sudhirdas K
;; APPLICANT: Shinkets, Richard A
;; APPLICANT: Rastelli, Luca
;; APPLICANT: Zerhusen, Bryan D
;; APPLICANT: Mezes, Peter S
;; TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the
;; FILE REFERENCE: 15966-609
;; CURRENT APPLICATION NUMBER: US/09/730,617
;; CURRENT FILING DATE: 2000-12-05
;; PRIOR APPLICATION NUMBER: 60/169,056
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: 60/169,886
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/169,866
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/170,252
;; PRIOR FILING DATE: 1999-12-10
;; PRIOR APPLICATION NUMBER: 60/175,740
;; PRIOR FILING DATE: 2000-01-12
;; NUMBER OF SEQ ID NOS: 100
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 46
;; LENGTH: 140
;; TYPE: PRT
;; ORGANISM: Carassius auratus
US-09-730-617-46
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Query Match          30.8%; Score 303; DB 10; Length 140;
Best Local Similarity 54.3%; Pred. No. 4.2e-18;
Matches 51; Conservative 16; Mismatches 27; Indels 0; Gaps 0;
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```
OY 31 PRRCRPNATLAVEKEGCVICITVNTTICAGYCPMTRVLOGVLPALPOVCNTRDVFES 90
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DB 27 PCEPVEIVAVEKEGCPKCLVLTQTTCSGCLTKEPVKSPSTVYOHVCTYRDVAYET 86
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 91 IRLPGCPRGVNPVSYAVALSOCALCRSTTDC 124
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 87 VRLPDCPGVDPHITYPVALSCHGCPCKRTSSTD 120
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```
RESULT 14
US-09-730-617-45
;; Sequence 45, Application US/09730617
;; Patent No. US20020068279A1
;; GENERAL INFORMATION:
;; APPLICANT: Burgess, Catherine E
;; APPLICANT: Prayaga, Sudhirdas K
;; APPLICANT: Shinkets, Richard A
;; APPLICANT: Rastelli, Luca
;; APPLICANT: Zerhusen, Bryan D
;; APPLICANT: Mezes, Peter S
;; TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the
;; FILE REFERENCE: 15966-609
;; CURRENT APPLICATION NUMBER: US/09/730,617
;; CURRENT FILING DATE: 2000-12-05
;; PRIOR APPLICATION NUMBER: 60/169,056
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: 60/169,886
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Job time : 6.77622 secs

;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/169,866
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/170,252
;; PRIOR FILING DATE: 1999-12-10
;; PRIOR APPLICATION NUMBER: 60/175,740
;; PRIOR FILING DATE: 2000-01-12
;; NUMBER OF SEQ ID NOS: 100
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 45
;; LENGTH: 144
;; TYPE: prt
;; ORGANISM: Homo sapiens
US-09-730-617-45

Query Match 30.8%; Score 303; DB 10; Length 144;
Best Local Similarity 54.3%; Pred. No. 4.3e-18;
Matches 51; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

OY 31 PRCRPINATLAVEKGCPCVITVNTTICAGYCPMTWRYLQGLPALPQVVCNRYDRFPES 90
Db 31 PRCRPVNETVAVEKGCPCVITVNTTICAGYCPMTWRYLQGLPALPQVVCNRYDRFPES 90
OY 91 IRLPGCPRGVNPVSYVALSCCALCRSTTDC 124
Db 91 VRLPDCPPGVDPHTYVVALSCDCSLCTMTSDC 124

RESULT 15
US-09-730-617-38
;; Sequence 38; Application US/09730617
;; Patent No. US20020068279A1
;; GENERAL INFORMATION:
;; APPLICANT: Burgess, Catherine E
;; APPLICANT: Prayaga, Sudhirdas K
;; APPLICANT: Shinkets, Richard A
;; APPLICANT: Rastelli, Luca
;; APPLICANT: Zerhusen, Bryan D
;; APPLICANT: Mezes, Peter S
;; TITLE OF INVENTION: No. US20020068279A1e1 Proteins and Nucleic Acids Encoding the Sam
;; FILE REFERENCE: 15966-609
;; CURRENT APPLICATION NUMBER: US/09/730,617
;; CURRENT FILING DATE: 2000-12-05
;; PRIOR APPLICATION NUMBER: 60/169,056
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: 60/169,886
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/169,866
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/170,252
;; PRIOR FILING DATE: 1999-12-10
;; PRIOR APPLICATION NUMBER: 60/175,740
;; PRIOR FILING DATE: 2000-01-12
;; NUMBER OF SEQ ID NOS: 100
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 38
;; LENGTH: 116
;; TYPE: prt
;; ORGANISM: Homo sapiens
US-09-730-617-38

Query Match 27.0%; Score 265.5; DB 10; Length 116;
Best Local Similarity 50.5%; Pred. No. 3.6e-15;
Matches 48; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

OY 29 LRRPCHPINATLAVEKGCPCVITVNTTICAGYCPMTWRYLQGLPALPQVVCNRYDRVF 88
Db 23 LRP-CVLVNETVAVEKGCPCVITVNTTICAGYCPMTWRYLQGLPALPQVVCNRYDRVF 88
OY 89 ESIRLPGCPRGVNPVSYVALSCCALCRSTTDC 123
Db 82 ETRLPDCADGVDPHTYVVALSCDCSLCTMTSDC 116

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OM protein - protein search, using sw model

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485.478 Million cell updates/sec

Title: US-09-787-494-2
Perfect score: 984
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	795	80.8	265	4	US-08-918-288-39
3	795	80.8	265	4	US-09-282-357-3
4	795	80.8	265	4	US-09-282-357-39
5	793	80.6	145	1	US-08-475-213-10
6	793	80.6	145	2	US-08-395-238-2
7	793	80.6	145	4	US-09-142-320-12
8	793	80.6	145	4	US-09-142-320-13
9	793	80.6	145	4	US-09-142-320-14
10	793	80.6	145	4	US-09-142-320-15
11	793	80.6	145	4	US-08-918-288-68
12	793	80.6	145	4	US-09-282-357-68
13	793	80.6	145	4	US-08-908-371B-1
14	790	80.3	165	2	US-08-709-924-2
15	790	80.3	165	2	US-08-709-925-2
16	790	80.3	165	4	US-08-709-948-2
17	789	80.2	181	4	US-08-918-288-36
18	789	80.2	181	4	US-09-282-357-36
19	787	80.0	145	1	US-08-425-673-1
20	787	80.0	145	1	US-08-425-673-2
21	787	80.0	145	1	US-08-238-189B-1
22	785	79.8	145	4	US-09-142-320-16
23	773	78.6	145	4	US-09-142-320-11
24	772	78.5	145	4	US-09-142-320-4
25	767	77.9	307	4	US-08-804-166-4
26	767	77.9	307	4	US-08-910-991-4
27	767	77.9	336	4	US-08-804-166-8

28	767	77.9	336	4	US-08-910-991-8	Sequence 8, Appl
29	766	77.8	145	1	US-08-425-673-10	Sequence 10, Appl
30	644	65.4	234	4	US-08-918-288-6	Sequence 6, Appl
31	644	65.4	234	4	US-09-282-357-6	Sequence 6, Appl
32	629	63.9	114	4	US-08-918-288-69	Sequence 69, Appl
33	629	63.9	114	4	US-09-282-357-69	Sequence 69, Appl
34	578	58.7	234	4	US-08-918-288-24	Sequence 24, Appl
35	578	58.7	234	4	US-09-282-357-24	Sequence 24, Appl
36	565	57.4	114	1	US-08-425-673-9	Sequence 9, Appl
37	557	56.6	114	1	US-08-425-673-7	Sequence 7, Appl
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41	549	55.8	234	4	US-09-282-357-21	Sequence 21, Appl
42	545	55.4	237	4	US-08-918-288-18	Sequence 18, Appl
43	545	55.4	237	4	US-09-282-357-18	Sequence 18, Appl
44	540	54.9	114	4	US-08-918-288-71	Sequence 71, Appl
45	540	54.9	114	4	US-09-282-357-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-08-918-288-3
; Sequence 3, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/282,357
; FILING DATE:
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-918-288-3

Db 82 VFESIRLPGCGRGVNPVSYAVALSCOCALCRSTTDCGPKDHLTCDPRFODSSSS 141
OY 146 KAPPSLPSRSLPGSDPTPLPQGS 171
Db 142 KAPPSLPSRSLPGSDPTPLPQGS 167

RESULT 4
US-09-282-357-39

; Sequence 39, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1868
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282.357
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/918,288
; FILING DATE: 25 AUG-1997
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-282-357-39

Query Match 80.8%; Score 795; DB 4; Length 265;
Best Local Similarity 99.3%; Pred. No. 2.3e-64;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 26 KEPLRRCRPIINATLAVEGCGPCVITVNTTCAGYCPMTRVLOGVLPALPOVVCNYRD 85
Db 22 KEPLRRCRPIINATLAVEGCGPCVITVNTTCAGYCPMTRVLOGVLPALPOVVCNYRD 81
OY 86 VFESIRLPGCGRGVNPVSYAVALSCOCALCRSTTDCGPKDHLTCDPRFODSSSS 145
Db 82 VFESIRLPGCGRGVNPVSYAVALSCOCALCRSTTDCGPKDHLTCDPRFODSSSS 141
OY 146 KAPPSLPSRSLPGSDPTPLPQGS 171

Db 142 KAPPSLPSRSLPGSDPTPLPQGS 167

RESULT 5
US-08-475-213-10

; Sequence 10, Application US/08475213
; Patent No. 5783674
; GENERAL INFORMATION:
; APPLICANT: Geysen, Hendrik M.
; TITLE OF INVENTION: Method for the use and Synthesis of
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,213
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/752,437
; FILING DATE: 06-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO pct/au90/00062
; FILING DATE: 16-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P02788/89
; FILING DATE: 17-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
; REGISTRATION NUMBER: 31259
; REFERENCE/DOCKET NUMBER: 0240.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2706
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-475-213-10

Query Match 80.6%; Score 793; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 26 KEPLRRCRPIINATLAVEGCGPCVITVNTTCAGYCPMTRVLOGVLPALPOVVCNYRD 85
Db 2 KEPLRRCRPIINATLAVEGCGPCVITVNTTCAGYCPMTRVLOGVLPALPOVVCNYRD 61
OY 86 VFESIRLPGCGRGVNPVSYAVALSCOCALCRSTTDCGPKDHLTCDPRFODSSSS 145
Db 62 VFESIRLPGCGRGVNPVSYAVALSCOCALCRSTTDCGPKDHLTCDPRFODSSSS 121
OY 146 KAPPSLPSRSLPGSDPTPLPQGS 169
Db 122 KAPPSLPSRSLPGSDPTPLPQGS 145
RESULT 6
US-08-395-238-2
; Sequence 2, Application US/08395238

Patent No. 5864488
GENERAL INFORMATION:
APPLICANT: ISSACS, Neil William
APPLICANT: LAPTHORN, Adrian Jonathan
APPLICANT: HARRIS, Deborah Claire
TITLE OF INVENTION: THREE DIMENSIONAL HORMONE STRUCTURE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: AKZO NOBEL PATENT DEPARTMENT
STREET: 1300 PICCARD DRIVE, SUITE 206
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: UNITED STATES
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,238
FILING DATE: 24-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9403600.1
FILING DATE: 24-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM M. BLACKSTONE
REGISTRATION NUMBER: 29,722
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BETA-SUBUNIT HUMAN CHORIONIC GONADOTROPIN
US-08-395-238-2

Query Match 80.6%; Score 793; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KEPLRRCRPI NATLAVEKGCPCITVNTTICAGYCPMTKRVLGVLPAIPQVVCNTRD 85
Db 2 KEPLRRCRPI NATLAVEKGCPCITVNTTICAGYCPMTKRVLGVLPAIPQVVCNTRD 61
Qy 86 VFESIRLPGCPRGVNPVSYAVALSCCALCRSTTDCGPKDHP LTCDDPRFQDSSSS 145
Db 62 VFESIRLPGCPRGVNPVSYAVALSCCALCRSTTDCGPKDHP LTCDDPRFQDSSSS 121
Qy 146 KAPPSLPSRLPGSDPTPLPQ 169
Db 122 KAPPSLPSRLPGSDPTPLPQ 145

RESULT 7
US-09-142-320-12
Sequence 12, Application US/09142320
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique
APPLICANT: Bidart, Jean-Michel
APPLICANT: Vidaud, Michel
TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
FILE REFERENCE: 065691/0140
CURRENT APPLICATION NUMBER: US/09/142,320
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/FR97/00361

EARLIER FILING DATE: 1997-02-28
EARLIER APPLICATION NUMBER: FR 96 02683
EARLIER FILING DATE: 1996-03-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 145
TYPE: PRT
ORGANISM: human
US-09-142-320-12

Query Match 80.6%; Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KEPLRRCRPI NATLAVEKGCPCITVNTTICAGYCPMTKRVLGVLPAIPQVVCNTRD 85
Db 2 KEPLRRCRPI NATLAVEKGCPCITVNTTICAGYCPMTKRVLGVLPAIPQVVCNTRD 61
Qy 86 VFESIRLPGCPRGVNPVSYAVALSCCALCRSTTDCGPKDHP LTCDDPRFQDSSSS 145
Db 62 VFESIRLPGCPRGVNPVSYAVALSCCALCRSTTDCGPKDHP LTCDDPRFQDSSSS 121
Qy 146 KAPPSLPSRLPGSDPTPLPQ 169
Db 122 KAPPSLPSRLPGSDPTPLPQ 145

RESULT 8
US-09-142-320-13
Sequence 13, Application US/09142320
Patent No. 6194154
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique
APPLICANT: Bidart, Jean-Michel
APPLICANT: Vidaud, Michel
APPLICANT: Lazari, Vladimir
TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
FILE REFERENCE: 065691/0140
CURRENT APPLICATION NUMBER: US/09/142,320
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/FR97/00361
EARLIER FILING DATE: 1997-02-28
EARLIER APPLICATION NUMBER: FR 96 02683
EARLIER FILING DATE: 1996-03-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 145
TYPE: PRT
ORGANISM: human
US-09-142-320-13

Query Match 80.6%; Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KEPLRRCRPI NATLAVEKGCPCITVNTTICAGYCPMTKRVLGVLPAIPQVVCNTRD 85
Db 2 KEPLRRCRPI NATLAVEKGCPCITVNTTICAGYCPMTKRVLGVLPAIPQVVCNTRD 61
Qy 86 VFESIRLPGCPRGVNPVSYAVALSCCALCRSTTDCGPKDHP LTCDDPRFQDSSSS 145
Db 62 VFESIRLPGCPRGVNPVSYAVALSCCALCRSTTDCGPKDHP LTCDDPRFQDSSSS 121
Qy 146 KAPPSLPSRLPGSDPTPLPQ 169
Db 122 KAPPSLPSRLPGSDPTPLPQ 145

RESULT 9
US-09-142-320-14
Sequence 14, Application US/09142320

Patent No. 6194154
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique
APPLICANT: Bidart, Jean-Michel
APPLICANT: Vidard, Michel
APPLICANT: Lazar, Viadimir
TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
FILE REFERENCE: 065691/0140
CURRENT APPLICATION NUMBER: US/09/142,320
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/FR97/00361
EARLIER FILING DATE: 1997-02-28
EARLIER APPLICATION NUMBER: FR 96 02683
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 145
TYPE: PRT
ORGANISM: human
US-09-142-320-14

Query Match 80.6%; Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPIATLAVEKEGCPVCTVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 85
DB 2 KEPLRRCRPIATLAVEKEGCPVCTVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 61
QY 86 VFESIRLPGCGPVNVVSYAVALSCQCALCRSTTDCGPGKDPHPLTCDPFRFODSSSS 145
DB 62 VFESIRLPGCGPVNVVSYAVALSCQCALCRSTTDCGPGKDPHPLTCDPFRFODSSSS 121
QY 146 KAPPSLPSRLPGSDPTILPO 169
DB 122 KAPPSLPSRLPGSDPTILPO 145

RESULT 10
US-09-142-320-15
Sequence 15, Application US/09142320
Patent No. 6194154
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique
APPLICANT: Bidart, Jean-Michel
APPLICANT: Vidard, Michel
APPLICANT: Lazar, Viadimir
TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
FILE REFERENCE: 065691/0140
CURRENT APPLICATION NUMBER: US/09/142,320
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/FR97/00361
EARLIER FILING DATE: 1997-02-28
EARLIER APPLICATION NUMBER: FR 96 02683
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 145
TYPE: PRT
ORGANISM: human
US-09-142-320-15

Query Match 80.6%; Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPIATLAVEKEGCPVCTVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 85
DB 2 KEPLRRCRPIATLAVEKEGCPVCTVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 61
QY 86 VFESIRLPGCGPVNVVSYAVALSCQCALCRSTTDCGPGKDPHPLTCDPFRFODSSSS 145

DB 62 VFESIRLPGCGPVNVVSYAVALSCQCALCRSTTDCGPGKDPHPLTCDPFRFODSSSS 121
QY 146 KAPPSLPSRLPGSDPTILPO 169
DB 122 KAPPSLPSRLPGSDPTILPO 145

RESULT 11
US-08-918-288-68
Sequence 68, Application US/08918288
Patent No. 623890
GENERAL INFORMATION:
APPLICANT: BOYME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTER
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-918-288-68

Query Match 80.6%; Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.8e-64;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPIATLAVEKEGCPVCTVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 85
DB 2 KEPLRRCRPIATLAVEKEGCPVCTVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 61
QY 86 VFESIRLPGCGPVNVVSYAVALSCQCALCRSTTDCGPGKDPHPLTCDPFRFODSSSS 145
DB 62 VFESIRLPGCGPVNVVSYAVALSCQCALCRSTTDCGPGKDPHPLTCDPFRFODSSSS 121
QY 146 KAPPSLPSRLPGSDPTILPO 169
DB 122 KAPPSLPSRLPGSDPTILPO 145

RESULT 12

US-09-282-357-68

Sequence 68, Application US/09282357

Patent No. 6242580

GENERAL INFORMATION:

APPLICANT: BOIME, Irving

APPLICANT: MOYLE, William R.

TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE

TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET

NUMBER OF SEQUENCES: 83

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/282,357

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/918,288

FILING DATE: 25 AUG-1997

APPLICATION NUMBER: 08/853,524

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: 08/199,382

FILING DATE: 18-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29500-20050.25

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-867-1500

TELEFAX: 202-887-0763

TELEX:

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 145 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-282-357-68

Query Match

Best Local Similarity 80.6%; Score 793; DB 4; Length 145;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPIINATLAVEGECPCVITVNTTICAGYCPMTVRVLOGVLPALPOVVCNTRD 85

DB 2 KEPLRRCRPIINATLAVEGECPCVITVNTTICAGYCPMTVRVLOGVLPALPOVVCNTRD 85

QY 86 VRFESIRLPGCGRGVNPVSYAVALSQCACLCRRSTTDCGPGKDHPLTCDPRFODSSSS 145

DB 62 VRFESIRLPGCGRGVNPVSYAVALSQCACLCRRSTTDCGPGKDHPLTCDPRFODSSSS 145

QY 146 KAPPSLSPSPRLPGPSDPTLPQ 169

DB 122 KAPPSLSPSPRLPGPSDPTLPQ 145

RESULT 13

US-08-908-371B-1

Sequence 1, Application US/08908371B

Patent No. 6331610

GENERAL INFORMATION:

APPLICANT: Bourinbalar, Aldar S.

TITLE OF INVENTION: A Method for Preventing and Treating

TITLE OF INVENTION: Aids and HIV Infection Using Select Peptides From the

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Metatron, Inc.

STREET: 367 Bay Shore Road

CITY: Deer Park

STATE: New York

COUNTRY: United States of America

ZIP: 11729

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 in. diskette (1.44megabytes)

COMPUTER: IBM Compatible PC

OPERATING SYSTEM: Windows 95

SOFTWARE: WORD 6.0 ASCII TEXT CONVERSION ONLY

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,371B

FILING DATE: 07-AUG-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/044,937

FILING DATE: 25-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: COLEMAN, HENRY D.

REGISTRATION NUMBER: 32,559

REFERENCE/DOCKET NUMBER: M31-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 679-0090

TELEFAX: (212) 679-9121

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 145 Amino Acid Units

TYPE: Amino Acid

STRANDEDNESS: Single Stranded

TOPOLOGY: Linear

MOLECULE TYPE: Protein Subunit

DESCRIPTION: Amino Acid Corresponding to Beta Subunit

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE: Sequence

IMMEDIATE SOURCE: N/A

POSITION IN GENOME: N/A

FEATURE:

NAME/KEY: 145 Units of Beta Subunit of Human Chorionic

NAME/KEY: Gonadotropin

LOCATION: N/A

IDENTIFICATION METHOD: Sequencing

PUBLICATION INFORMATION:

AUTHORS: CARLSEN, Robert B.,

AUTHORS: BAH, Ohm P.,

AUTHORS: SWAMINATHAN, N.

TITLE: HUMAN CHORIONIC GONADOTROPIN

JOURNAL: THE JOURNAL OF BIOLOGICAL CHEMISTRY

VOLUME: 248

PAGES: 6810-6825

DATE: 1973

US-08-908-371B-1

Query Match

Best Local Similarity 80.6%; Score 793; DB 4; Length 145;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPIINATLAVEGECPCVITVNTTICAGYCPMTVRVLOGVLPALPOVVCNTRD 85

DB 2 KEPLRRCRPIINATLAVEGECPCVITVNTTICAGYCPMTVRVLOGVLPALPOVVCNTRD 85

QY 86 VRFESIRLPGCGRGVNPVSYAVALSQCACLCRRSTTDCGPGKDHPLTCDPRFODSSSS 145

DB 62 VRFESIRLPGCGRGVNPVSYAVALSQCACLCRRSTTDCGPGKDHPLTCDPRFODSSSS 145

QY 146 KAPPSLSPSPRLPGPSDPTLPQ 169

Db 122 KAPPSLPSRLPGSDPTILPQ 145

RESULT 14

US-08-709-924-2

Sequence 2, Application US/08709924

Patent No. 5968513

GENERAL INFORMATION:

APPLICANT: Gallo, Robert C.

APPLICANT: Bryant, Joseph

APPLICANT: Lunardi-Iskandar, Yanto

TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS

TITLE OF INVENTION: USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,924.

FILING DATE: 09-SEP-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 8769-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 165 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-709-924-2

Query Match 80.3%; Score 790; DB 2; Length 165;

Best Local Similarity 99.3%; Pred. No. 3.8e-64;

Matches 143; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTFRLVGLPALPOVCNRYD 85

Db 22 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTFRLVGLPALPOVCNRYD 81

QY 86 VRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDCGPGKDHPLTCDDPRFQDSSSS 145

Db 82 VRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDCGPGKDHPLTCDDPRFQDSSSS 141

QY 146 KAPPSLPSRLPGSDPTILPQ 169

Db 142 KAPPSLPSRLPGSDPTILPQ 165

RESULT 15

US-08-709-925-2

Sequence 2, Application US/08709925

Patent No. 5997871

GENERAL INFORMATION:

APPLICANT: Gallo, Robert C.

APPLICANT: Bryant, Joseph

APPLICANT: Lunardi-Iskandar, Yanto

TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY

TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,925

FILING DATE: 09-SEP-1996

CLASSIFICATION: 512

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 8769-017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 165 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-709-925-2

Query Match 80.3%; Score 790; DB 2; Length 165;

Best Local Similarity 99.3%; Pred. No. 3.8e-64;

Matches 143; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 26 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTFRLVGLPALPOVCNRYD 85

Db 22 KEPLRRCRPI NATLAVEKEGCPVCTVNTTICAGYCPMTFRLVGLPALPOVCNRYD 81

QY 86 VRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDCGPGKDHPLTCDDPRFQDSSSS 145

Db 82 VRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDCGPGKDHPLTCDDPRFQDSSSS 141

QY 146 KAPPSLPSRLPGSDPTILPQ 169

Db 142 KAPPSLPSRLPGSDPTILPQ 165

Search completed: November 20, 2002, 17:29:32
Job time : 11.7273 secs

GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 17.035 Seconds

(without alignments)
1422.126 Million cell updates/sec

Title: us-09-787-494-4

Perfect score: 1347

Sequence: 1 MRPSIFTAVLEAASALAA.....LPGPSDPILPQTSNNHHN 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	793	58.9	165	1	KTTHUB
2	785	58.3	145	2	Choriogonadotropin beta-gonadotropin
3	651	48.3	165	1	KTTHUB
4	540	40.1	141	1	Choriogonadotropin
5	444	33.0	169	1	Choriogonadotropin
6	435	32.3	141	1	Choriogonadotropin
7	435	32.3	141	1	Choriogonadotropin
8	432	32.1	141	1	Choriogonadotropin
9	431	32.0	139	2	Choriogonadotropin
10	429.5	31.9	165	1	Choriogonadotropin
11	427	31.7	119	2	Choriogonadotropin
12	425	31.6	141	1	Choriogonadotropin
13	421	31.3	141	1	Choriogonadotropin
14	418	31.0	138	2	Choriogonadotropin
15	407	30.2	118	2	Choriogonadotropin
16	406	30.1	118	2	Choriogonadotropin
17	303	22.5	144	1	Choriogonadotropin
18	301	22.3	141	1	Choriogonadotropin
19	301	22.3	141	1	Choriogonadotropin
20	291	21.6	142	1	Choriogonadotropin
21	288	21.4	142	2	Choriogonadotropin
22	278	20.6	142	2	Choriogonadotropin
23	276.5	20.5	113	1	Choriogonadotropin
24	273	20.3	140	2	Choriogonadotropin
25	273	20.3	142	2	Choriogonadotropin
26	269	20.0	128	2	Choriogonadotropin
27	269	20.0	158	2	Choriogonadotropin
28	265	19.7	112	2	Choriogonadotropin
29	260	19.3	159	2	Choriogonadotropin

30	258	19.2	166	2	luteinizing hormone
31	255.5	19.0	80	2	testicular luteinizing hormone
32	255	18.9	147	2	gonadotropin II be
33	243	18.0	138	1	thyrotropin beta c
34	243	18.0	138	1	thyrotropin beta c
35	242	18.0	138	1	thyrotropin beta c
36	240	17.8	138	1	thyrotropin beta c
37	239	17.7	138	1	thyrotropin beta c
38	229	17.0	136	2	gonadotropin beta c
39	227	16.9	118	1	gonadotropin II be
40	226	16.8	120	2	gonadotropin beta c
41	222	16.5	130	2	gonadotropin beta c
42	218	16.2	130	2	gonadotropin beta c
43	215	16.0	129	1	gonadotropin beta c
44	215	16.0	129	1	gonadotropin beta c
45	209	15.5	129	2	gonadotropin beta c

ALIGNMENTS

RESULT 1

KTTHUB

N:Alternative names: beta-gonadotropin; Choriogonadotropin beta chain

C:Species: Homo sapiens (man)

C>Date: 23-Oct-1981 #sequence, revision 23-Oct-1981 #text, change 08-Dec-2000

C:Accession: A93230; 169972; 155224; 155250; 170007; 170008; A92303; A92181; A92142;

R:Pidder, J.C.; Goodman, H.M.

Nature 286, 684-687, 1980

A:Title: The cDNA for the beta-subunit of human choriogonadotropin suggests evolu

A:Reference number: A93230; M01D:81012134; PMID:6774259

A:Accession: A93230

A:Molecule type: mRNA

A:Residues: 1-165 <PID>

A:Cross-references: GB:J00117; GB:M3555; GB:M54963; NID:g180436; PIDN:AAA6690.1; PI

R:Pollicastro, P.; Ovitte, C.E.; Hoshina, M.; Fukunaka, H.; Boonchu, M.R.; Boime, I.

J. Biol. Chem. 258, 11492-11499, 1983

A:Title: The beta subunit of human choriogonadotropin is encoded by multiple gene

A:Reference number: 155224; M01D:84008141; PMID:6194155

A:Accession: 169972

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-165 <POL>

A:Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453

A:Note: clone CG-beta-e

A:Accession: 155224

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-23, 'M', '25-136', 'A', '138-165' <P02>

A:Cross-references: GB:K03183; NID:g180442; PIDN:AAA53287.1; PID:g180444

A:Note: clone CG-beta-a

R:Pollicastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.

J. Biol. Chem. 261, 5907-5916, 1986

A:Title: A map of the hCG beta-LH gene cluster.

A:Reference number: 155250; M01D:86195987; PMID:2422163

A:Accession: 155250

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <P03>

A:Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088

A:Note: CG-beta-6 gene

A:Accession: 170007

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <P04>

A:Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089

A:Note: CG-beta-6 gene

A:Accession: 170008

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090

A>Note: Cg-beta-7 gene
R:Birken, S.; Featherston, J.; Canfield, R.; Boime, I.
J. Biol. Chem. 256, 1816-1823, 1981
A>Title: The amino acid sequences of the prepeptides contained in the alpha and beta sub
A:Accession: A92303
A:Molecule type: protein
A:Residues: 1-20 <BIR>
A>Note: the identity of the residue at position 19 could not be determined
R:Morgan, F.J.; Birken, S.; Canfield, R.E.
J. Biol. Chem. 250, 5247-5258, 1975
A>Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and
A:Accession: A92181
A:Molecule type: protein
A:Residues: 21-165 <MOK>
R:Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
J. Biol. Chem. 248, 6810-6827, 1973
A:Reference number: A92142; MUID:74011267; PMID:4795659
A:Accession: A92142
A:Molecule type: protein
R:Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
Chinese Biochem. J. 6, 558-562, 1990
A>Title: The immunological characteristics of the enzymatic fragments of human chorionic
A:Accession: PC1016
A:Molecule type: protein
A:Residues: 21-165 <SHI>
R:Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichevsky, A.;
Endocrinology 123, 572-583, 1988
A>Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pregna
A:Accession: A61097; MUID:88254680; PMID:2454811
A:Molecule type: protein
A:Residues: 26-32, 'X', '34-49', 'X', '51-60', '75-112' <B12>
R:Kardana, A.; Beggs, K.D.; Coles, B.; Read, D.; Taylor, M.
Br. J. Cancer 67, 686-692, 1993
A>Title: Characterisation of UGP and its relationship with beta-core fragment.
A:Accession: B56873; MUID:93229246; PMID:8471426
A:Molecule type: protein
A:Residues: 26-28, 'X', '30-32', 'X', '34-42', 'X', '44-45', 'X', '47-48', '75-76', 'X', '78-91', 'G', '93-102' <K
A>Note: sequence modified after extraction from NCBI backbone
R:Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Luschader, J.W.; Canfield, R.E.; Machin,
Nature 369, 455-461, 1994
A>Title: Crystal structure of human chorionic gonadotropin.
A:Accession: A44674; MUID:94261179; PMID:8202136
R:Talnadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A>Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin an
A:Accession: 137231; MUID:84093590; PMID:6650962
A:Molecule type: DNA
A:Residues: 21-165 <RES>
A:Cross-references: EMBL:X00265; NID:931719; PIDN:CAA25068.1; PID:g1335075
C:Genetics:
A:Gene: GDB:CGS
A:Cross-references: GDB:119055; OMIM:118860
A:Map position: 19q13.3-19q13.3
A:Introns: 5/3; 61/3
A>Note: the choriongonadotropin beta chain locus contains six genes (or pseudogenes)
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status experimental <SIG>
F:21-165/Product: choriongonadotropin beta chain #status experimental <MAT>
F:29-77, 43-92, 46-130, 54-108, 58-110, 113-120/Disulfide Bonds: #status experimental

F:33, 50/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:138, 150/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:141, 147, 152, 158/Binding site: carbohydrate (Ser) (covalent) #status experimental
Query Match
Best Local Similarity 58.3%; Score 793; DB 1; Length 165;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 KEPLRRCPINATLAVEKEGCPVITVNTTCAGYCPTRVLOGLPALPOVCNRYD 160
DB 22 KEPLRRCPINATLAVEKEGCPVITVNTTCAGYCPTRVLOGLPALPOVCNRYD 160
QY 161 VFESIRLPGCPGVNPPVSYAVALSOCALCRSTTDCGPDHPLTCDPFDSSSS 220
DB 82 VFESIRLPGCPGVNPPVSYAVALSOCALCRSTTDCGPDHPLTCDPFDSSSS 220
QY 221 KAPPSLPSRRLPGSDPTLPQ 244
DB 142 KAPPSLPSRRLPGSDPTLPQ 165

RESULT 2
137231
beta-gonadotropin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
R:Talnadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A>Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
A:Accession: 137231; MUID:84093590; PMID:6650982
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-145 <RES>
A:Cross-references: EMBL:X00265; NID:929907; PIDN:CAA25069.1; PID:g1335012
C:Genetics:
A:Introns: 41/3
C:Superfamily: pituitary glycoprotein hormone beta chain

Query Match 58.3%; Score 785; DB 2; Length 145;
Best Local Similarity 99.3%; Pred. No. 2, 2e-55;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 101 KEPLRRCPINATLAVEKEGCPVITVNTTCAGYCPTRVLOGLPALPOVCNRYD 160
DB 2 KEPLRRCPINATLAVEKEGCPVITVNTTCAGYCPTRVLOGLPALPOVCNRYD 160
QY 161 VFESIRLPGCPGVNPPVSYAVALSOCALCRSTTDCGPDHPLTCDPFDSSSS 220
DB 62 VFESIRLPGCPGVNPPVSYAVALSOCALCRSTTDCGPDHPLTCDPFDSSSS 220
QY 221 KAPPSLPSRRLPGSDPTLPQ 244
DB 122 KAPPSLPSRRLPGSDPTLPQ 145

RESULT 3
KTBA
Choriongonadotropin beta chain precursor - olive baboon
C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-May-1999
R:Crawford, R.J.; Tregear, G.W.; Niall, H.D.
Gene 46, 161-169, 1986
A>Title: The nucleotide sequences of baboon chorionic gonadotropin beta-subunit genes
A:Reference number: A25808; MUID:87106851; PMID:2433190
A:Accession: A25808
A:Molecule type: mRNA
A:Residues: 1-165 <CRA>
A:Cross-references: GB:M14966; NID:9176572; PIDN:AAA5383.1; PID:g176573
C:Comment: There are at least five copies of CG-related genes and at least two of the
C:Superfamily: pituitary glycoprotein hormone beta chain

A:Reference number: A55952; MUID:95034847; PMID:7524670
A:Contents: annotation; glycosylation
A:Note: horse lutropin and chorionotropin beta chains have identical protein chains
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1.20/Domain: signal sequence #status predicted <SIG>
F:2.169/Product: chorionotropin beta chain #status experimental <MAT>
F:29-77,43-92,46-130,54-108,58-110,113-120/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match
Best Local Similarity 33.0%; Score 444; DB 1; Length 169;
Matches 86; Conservative 16; Mismatches 39; Indels 8; Gaps 2;

QY 103 PLRPRCPINATLAVERGECPCVCTVTTCAGYCPPTMREVLQGVLPALPOVVCNRRDVR 162
Db 24 PLRPLCRPINATLAVERGECPCITFTTSTICAGYCSMRVLPALPOVVCYHRLR 83
QY 163 FESIRLPCPCPGVNPVSVYVALSCCALCRSTTDCGGRKPHPLTCDPFRDSSSKA 222
Db 84 FASIRLPCPCPGVNPVSVYVALSCGRCGKRTDCCGVFRDQPLACAP--QASSSSKD 140
QY 223 PPSPSPSRPLRGP-----SDTPIIPQTS 246
Db 141 PPSPPLTSTPTTPGASRRSHPLPIKTS 169

RESULT 6

UTR0B
Lutropin beta chain precursor - bovine
M:Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C:Species: Bos primigenius laurus (cattle)
C:Date: 30-Jun-1987 #sequence, revision 30-Jun-1987 #text_change 24-Nov-1999
A:Accession: A92518; A92518; A91212; A01409
J. Riviglin, J.B. Silver, B.J. Thomson, A.R. Nilson, J.H.
A:Title: The gene for the beta subunit of bovine luteinizing hormone encodes a gonadotro
A:Reference number: A92534; MUID:85207729; PMID:2987241
A:Accession: A92534
A:Molecule type: DNA
A:Residues: 1-141 <VR>
A:Cross-references: GB:M1506; NID:g163298; PIDN:AAH59267.1; PID:g163299
J. Maurer, R.A.

J. Biol. Chem. 260, 4684-4687, 1985
A:Title: Analysis of several bovine lutropin beta subunit cDNAs reveals heterogeneity in
A:Reference number: A92518; MUID:85182575; PMID:3838746
A:Accession: A92518
A:Molecule type: mRNA
A:Residues: 3-111, 'S', '113-141' <MAU>
A:Cross-references: GB:M10077; NID:g163300; PIDN:AAA30623.1; PID:g163301
R. Maghniin-Rogister, G. Hennen, G.

Eur. J. Biochem. 39, 235-253, 1973
A:Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and
A:Reference number: A91212; MUID:74075724; PMID:4770795
A:Accession: A91212
A:Molecule type: Protein
A:Residues: 21-73, 'E', '75-121, 'PG', '124-125, 'E', '127-139' <MAG>
A:Note: some carboxyl-terminal heterogeneity was found
A:Genetics:
A:Insertions: 5/3; 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
F:1.20/Domain: signal sequence #status predicted <SIG>
F:2.169/Product: lutropin beta chain #status experimental <LUB>
F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match
Best Local Similarity 32.3%; Score 435; DB 1; Length 141;
Matches 75; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 103 PLRPRCPINATLAVERGECPCVCTVTTCAGYCPPTMREVLQGVLPALPOVVCNRRDVR 162

RESULT 7

UTR0B
Lutropin beta chain precursor - sheep
M:Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; lutein
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 24-Apr-1984 #sequence, revision 19-Jan-2001 #text_change 19-Jan-2001
A:Accession: I46949; S09232; A92110; A90053; B61098; A01500
M. Brown, P. McNeilly, J.R. Wallace, R.M. McNeilly, A.S. Clark, A.J.
A:Title: Characterization of the ovine LH beta-subunit gene: the promoter directs go
A:Reference number: I46949; MUID:93351742; PMID:8349025
A:Accession: I46949
A:Molecule type: DNA
A:Residues: 1-141 <BRO>
A:Cross-references: GB:S64695; NID:g408240; PIDN:AAH27819.1; PID:g408241
R. d'Angelo-Bernard, G. Moumni, M. Jutisz, M. Counts, R.

Nucleic Acids Res. 18, 2175, 1990
A:Title: Cloning and sequence analysis of the cDNA for the precursor of the beta subu
A:Reference number: S09232; MUID:90245669; PMID:2336396
A:Accession: S09232
A:Molecule type: mRNA
A:Residues: 1-58, 'V', '60-62, 'Q', '64-141' <ANG>
A:Cross-references: EMBL:X52488; NID:g1319; PIDN:CAA36729.1; PID:g1320
J. Liu, W.K. Nahm, H.S. Sweeney, H. Pakkoff, H. Li, C.H.

J. Biol. Chem. 247, 4365-4381, 1972
A:Title: The primary structure of ovine luteinizing hormone. II. The amino acid seque
A:Reference number: A92110; MUID:72211145; PMID:4556309
A:Accession: A92110
A:Molecule type: Protein
A:Residues: 21-121, 'PG', '124-125, 'E', '127-139' <LUD>
R. Salram, M.R. T.S.A. Pakkoff, H. Li, C.H.

Arch. Biochem. Biophys. 153, 572-586, 1972
A:Title: The primary structure of ovine luteinizing hormone. I. The amino acid seque
A:Reference number: A90053; MUID:73190033; PMID:4575435
A:Accession: A90053
A:Molecule type: Protein
A:Residues: 21-29, 'P', '72-80, 'Q', '82-121, 'PG', '124-125, 'E', '127-139' <SAI>
R. Nomura, K. Tsunashima, S. Ohmura, K. Sakiyama, F. Shizume, K.

Endocrinology 123, 700-712, 1988
A:Title: Renotropic activity in ovine luteinizing hormone isoform(s).
A:Reference number: A61098; MUID:88283534; PMID:2456202
A:Accession: B61098
A:Molecule type: Protein
A:Residues: 21-39, 'N', '41-49, '64-78, 'V', '80-82, '84-106, '115-121, 'PG', '124-138' <NOM>
A:Note: this form was designated form beta-3, forms beta-1 and beta-2 each lack sever
A:Genetics:
A:Insertions: 5/3; 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
F:1.20/Domain: signal sequence #status predicted <SIG>
F:2.169/Product: lutropin beta chain #status experimental <LUB>
F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acet
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match
Best Local Similarity 32.3%; Score 435; DB 1; Length 141;
Matches 75; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 103 PLRPRCPINATLAVERGECPCVCTVTTCAGYCPPTMREVLQGVLPALPOVVCNRRDVR 162
Db 24 PLRPLCRPINATLAVERGECPCITFTTSTICAGYCSMRVLPALPOVVCYHRLR 83
QY 163 FESIRLPCPCPGVNPVSVYVALSCCALCRSTTDCGGRKPHPLTCDPFRDSSSKA 222
Db 84 FASIRLPCPCPGVNPVSVYVALSCGRCGKRTDCCGVFRDQPLACAP--QASSSSKD 140

R: Tanaka, T.; Kita, H.; Murakami, T.; Narita, K.
J. Biochem. 92, 1681-1687, 1977

A: Title: Purification and amino acid sequence of mating factor from *Saccharomyces cerevisiae*

A: Reference number: A91943; MUID: 78087498; PMID: 340452

A: Accession: A91943

A: Molecule type: protein

A: Residues: 90-102 <TRANS>

A: Experimental source: strain X2180-1B

A: Gene: SGD:MF(ALPHA1); MFA1; MIPS:YPL187W

A: Cross-references: SGD:S0006108; MIPS:YPL187W

A: Map position: 16L

C: Function:

A: Description: mediates the conjugation process between the two mating types by inhibiting

C: Superfamily: mating hormone alpha precursor

C: Keywords: duplication; extracellular protein; glycoprotein; hormone; tandem repeat

F: 1-19/Domain: signal sequence #status predicted <SIG>

F: 84-102/103-123-124-144-145-165/Region: 21-residue repeats

F: 90-102/Product: mating pheromone alpha #status experimental <MAT1>

F: 111-123/Product: mating pheromone alpha #status experimental <MAT2>

F: 132-144/Product: mating pheromone alpha #status experimental <MAT3>

F: 153-165/Product: mating pheromone alpha #status experimental <MAT4>

F: 23,57,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 31.9%; Score 429.5; DB 1; Length 165;

Matches 91; Conservative 6; Mismatches 5; Indels 7; Gaps 2;

OY 1 MRPSPFPAVPAASSALAAVNTTDETAQPAEAVITGYSLDEDFVAVLPFSNSTN 60

DB 1 MRPSPFPAVPAASSALAAVNTTDETAQPAEAVITGYSLDEDFVAVLPFSNSTN 60

OY 61 NGLLFNTTASTIAAKEGSLKREAE--VEEDPGCRDKLEPRPR 107

DB 61 NGLLFNTTASTIAAKEGSLKREAE--VEEDPGCRDKLEPRPR 107

RESULT 11

A61465

Lutropin beta chain - rabbit

C: Species: *Oryctolagus cuniculus* (domestic rabbit)

C: Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-1995

C: Accession: A61465

R: Glenn, S.D.; Nahm, H.S.; Ward, D.N.

J. Protein Chem. 3, 259-273, 1984

A: Title: The amino acid sequence of the rabbit lutropin beta subunit.

A: Reference number: A61465

A: Accession: A61465

A: Status: Preliminary

A: Molecule type: protein

A: Residues: 1-119 <GLY>

A: Note: the sequence from Fig. 1 is inconsistent with that from the abstract in having 1

F: 11-36,25-59,28-90,40-112,74-102,92-95/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 31.7%; Score 427; DB 2; Length 119;

Matches 74; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

OY 103 PLRPRCPINATLAVERKEGCPVCIIVNTTICAGYCPMTRVLYGVLPALPOVNCNRYDVR 162

DB 6 PLRPRCPINATLAVERKEGCPVCIIVNTTICAGYCPMTRVLYGVLPALPOVNCNRYDVR 162

OY 163 FESIRLPGCPRVNPNVYVAVALSCQALCRSTTDCGKPRDHPVCTYREL 65

DB 66 FASIRLPGCPRVNPNVYVAVALSCQALCRSTTDCGKPRDHPVCTYREL 65

RESULT 12

UTPG

Lutropin beta chain precursor - pig

N: Alternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; Lutelutizing

C: Species: *Sus scrofa domestica* (domestic pig)

C: Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000

A: Accession: A48170; A30322; A01501; A60584

R: Ezesh, T.; Hirai, T.; Kato, T.; Wakabayashi, K.; Kato, Y.

J. Mol. Endocrinol. 5, 137-146, 1990

A: Title: The gene for the beta subunit of porcine LH: clusters of GC boxes and CACCC

A: Reference number: A48170; MUID: 91063934; PMID: 1701088

A: Accession: A48170

A: Molecule type: DNA

A: Residues: 1-141 <RZA>

A: Cross-references: GB:D00579; MUID: 9217693; PIDN: BAA00457.1; PID: 9217694

Mol. Cell. Endocrinol. 62, 47-53, 1989

A: Title: Cloning and DNA sequence analysis of the cDNA for the precursor of porcine 1

A: Reference number: A30322; MUID: 89306142; PMID: 2744222

A: Accession: A30322

A: Status: not compared with conceptual translation

A: Molecule type: mRNA

A: Residues: 1-141 <KAT>

R: Maghuln-Rogister, G.; Hennem, G.

Eur. J. Biochem. 39, 235-253, 1973

A: Title: Lutelutizing hormone. The primary structures of the beta-subunit from bovine

A: Reference number: A91212; MUID: 74075724; PMID: 4770795

A: Accession: A01501

A: Molecule type: protein

A: Residues: 21-29, '2', '31-39, 'D', '41-61, 'R', '63-82, 'T', '84-86, 'S', '88-121, 'PG', '124-133, 'P

A: Note: about half the chains lack one or both carboxyl-terminal leucines

R: Nomura, K.; Ohmura, K.; Nakamura, Y.; Horiba, N.; Shikura, Y.; Sato, Y.; Ujihara, Y.

Endocrinology 124, 712-719, 1989

A: Title: Porcine lutelutizing hormone isoform(s): relationship between their molecular

A: Reference number: A60584; MUID: 89107050; PMID: 2556317

A: Accession: A60584

A: Molecule type: protein

A: Residues: 21-31; 137-139 <NOM>

A: Note: the lutropin beta chain is heterogeneous at the carboxyl end; this form lacks

C: Geneticks:

A: Introns: 5/3; 61/73

C: Superfamily: pituitary glycoprotein hormone beta chain

C: Keywords: blocked amino end; glycoprotein; hormone

F: 1-20/Domain: signal sequence #status predicted <SIG>

F: 21-141/Product: lutropin beta chain #status predicted <SIG>

F: 21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #

F: 29-54, 43-77, 46-108, 58-130, 92-120, 110-113/Disulfide bonds: #status predicted

F: 33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

Best Local Similarity 31.6%; Score 425; DB 1; Length 141;

Matches 74; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

OY 103 PLRPRCPINATLAVERKEGCPVCIIVNTTICAGYCPMTRVLYGVLPALPOVNCNRYDVR 162

DB 24 PLRPRCPINATLAVERKEGCPVCIIVNTTICAGYCPMTRVLYGVLPALPOVNCNRYDVR 162

OY 163 FESIRLPGCPRVNPNVYVAVALSCQALCRSTTDCGKPRDHPVCTYREL 83

DB 84 FASIRLPGCPRVNPNVYVAVALSCQALCRSTTDCGKPRDHPVCTYREL 133

RESULT 13

JC4527

Lutelutizing hormone beta chain precursor - mouse

C: Species: *Mus musculus* (house mouse)

C: Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 16-Jul-1999

C: Accession: JC4527

R: Kumar, T.R.; Matzuk, M.M.

Gene 166, 335-336, 1995

A: Title: Cloning of the mouse gonadotropin beta-subunit-encoding genes, II. Structure

A: Reference number: JC4527; MUID: 96125216; PMID: 8543188

A: Accession: JC4527

A: Molecule type: mRNA

A: Residues: 1-141 <KUM>

A: Cross-references: GB:U25145; MUID: 9350344; PIDN: AAA92841.1; PID: 9350345

A: Experimental source: 1295VEV

C:Comment: This protein is co-produced with follicle-stimulating hormone in pituitary gonadotropin reproduction including gonadal growth, gametogenesis and steroidogenesis.

C:Genetics:

A:Gene: 1h beta

A:Introns: 5/3: 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: hormone; reproduction

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-141/Product: luteinizing hormone beta chain #status predicted <MAT>

Query Match 31.3%; Score 421; DB 2; Length 141;

Best Local Similarity 64.5%; Pred. No. 1.7e-26; Mismatches 24; Indels 0; Gaps 0;

Matches 71; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 103 PLRRCRPNATLAVEKEGCPVCTITNTTICAGYCPMTFRVLOGVLPALPQVWCNRYDVR 162

Db 24 PLRPLCRPNATLAEENECPCITFTTTSICAGYCPSMVRVLPALPVPVQPCYRHLA 83

QY 163 FESIRLPGCCPGVNPVSYAVALSOCALCRSTTDCGPKDHPITCDDP 212

Db 84 FASVRLPGCPGVDPVPSFVALSCRCGRCRLSSDCGGRPTQPMACDLP 133

RESULT 14

S00512

lutropin beta chain precursor - dog (fragment)

N:Alternate names: luteinizing hormone beta chain

C:Species: Canis lupus familiaris (dog)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

C:Accession: S00512

R:Wolfe, D.L.; Appleby, V.L.; Hjertild, K.; Baker, A.R.; Talmadge, K.

Nucleic Acids Res. 15, 10602, 1987

A:Title: Nucleic acid and amino acid sequences of dog beta-LH: comparison to rat, cow and

A:Reference number: S00512; MUID:88096605; PMID:3697104

A:Accession: S00512

A:Molecule type: mRNA

A:Residues: 1-138 <WOL>

A:Cross-References: EMBL:Y00518; NID:9907; PIDN:CAA68572.1; PID:g860906

C:Superfamily: pituitary glycoprotein hormone beta chain

F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>

F:18-138/Product: lutropin beta chain #status predicted <MAT>

F:26-51,40-74,43-105,55-127,89-117,107-110/Disulfide bonds: #status predicted

Query Match 31.0%; Score 418; DB 2; Length 138;

Best Local Similarity 66.4%; Pred. No. 2.9e-26; Mismatches 27; Indels 0; Gaps 0;

Matches 73; Conservative 10; Mismatches 27; Indels 0; Gaps 0;

QY 103 PLRRCRPNATLAVEKEGCPVCTITNTTICAGYCPMTFRVLOGVLPALPQVWCNRYDVR 162

Db 21 PLRPLCRPNATLAEENECPCITFTTTSICAGYCPSMVRVLPALPVPVQPCYRHLA 80

QY 163 FESIRLPGCCPGVNPVSYAVALSOCALCRSTTDCGPKDHPITCDDP 212

Db 81 FASIRLPGCCPGVDPVPSFVALSCRCGRCRLSSDCGGRPTQPMACDLP 130

RESULT 15

PNO139

lutropin beta chain - minke whale

N:Alternate names: luteinizing hormone beta chain

C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)

C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 08-Dec-1995

C:Accession: PNO139

R:Karasev, V.S.; Pankov, Y.A.

Biokhimiya 50, 1972-1986, 1985

A:Title: Amino acid sequence of reduced and carboxymethylated alpha- and beta-subunits of

A:Reference number: PNO138

A:Accession: PNO139

A:Molecule type: protein

A:Residues: 1-118 <KAR>

A>Note: article in Russian with English abstract

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: glycoprotein; hormone

F:9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted

F:13/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 30.2%; Score 407; DB 2; Length 118;

Best Local Similarity 56.0%; Pred. No. 1.8e-25; Mismatches 27; Indels 10; Gaps 1;

Matches 70; Conservative 18; Mismatches 27; Indels 10; Gaps 1;

QY 103 PLRRCRPNATLAVEKEGCPVCTITNTTICAGYCPMTFRVLOGVLPALPQVWCNRYDVR 162

Db 4 PLRPLCRPNATLAEABZACPCITFTTTSICAGYCPSMVRVLPALPVPVQPCYRHLA 63

QY 163 FESIRLPGCCPGVNPVSYAVALSOCALCRSTTDCGPKDHPITCDDPFRQSSSKA 222

Db 64 FASIRLPGCCPGVBPVPSFVALSCRCGRCRLSSDCGGRPTQPMACDLP 113

QY 223 PPPSL 227

Db 114 PREEL 118

Search completed: November 20, 2002, 17:30:08
Job time : 18.035 secs

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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:26 ; Search time 9.98601 Seconds

(without alignments)
1046.667 Million cell updates/sec

Title: US-09-787-494-4

Perfect score: 1347
Sequence: 1 MRPPSIFTAVLFAASSALAA.....LPGPSDTPILPOTSHHHHHH 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	58.9	165	1	CGHB_HUMAN
2	651	48.3	165	1	CGHB_PAPAN
3	540	40.1	141	1	LSHB_HUMAN
4	516.5	38.3	164	1	CGHB_CALUA
5	474	35.2	169	1	LSHB_EOUBU
6	459	34.1	169	1	LSHB_EOUAS
7	444	33.0	143	1	LSHB_FELCA
8	444	33.0	169	1	LSHB_HORSE
9	435	32.3	141	1	LSHB_BOVIN
10	432	32.1	141	1	LSHB_RAT
11	429.5	31.9	144	1	MEFAL_SACBA
12	429.5	31.9	165	1	MEFAL_YEAST
13	429.5	31.9	186	1	MEFAL_YEAST
14	426	31.6	141	1	LSHB_CERST
15	425	31.6	141	1	LSHB_PIG
16	425	31.6	141	1	LSHB_SHEEP
17	421	31.3	141	1	LSHB_MOUSE
18	418	31.0	138	1	LSHB_CANFA
19	407	30.2	118	1	LSHB_BALAC
20	406	30.1	118	1	LSHB_PHYCA
21	405	30.1	128	1	LSHB_PHOSU
22	402	29.8	138	1	LSHB_MACRU
23	393	29.2	141	1	LSHB_TRIUV
24	303	22.5	140	1	GTH2_CARAU
25	303	22.5	144	1	GTH2_CYPCA
26	301	22.3	141	1	GTH2_HYPMO
27	301	22.3	146	1	GTH2_CTERD
28	291	21.6	142	1	GTH2_ONCKE
29	288	21.4	140	1	GTH2_ONCMA
30	284	21.1	140	1	GTH2_ICTPU
31	283	21.0	138	1	GTH2_CLAGA
32	282	20.9	149	1	GTH2_CLUPA
33	278	20.6	142	1	GTH2_ONCTS

34	276.5	20.5	113	1	GTHB_MURCI	P12837 murenesox
35	273	20.3	140	1	GTH2_ANGAN	P27767 anguilla an
36	273	20.3	142	1	GTH2_CORAU	P48251 coregonus a
37	269	20.0	128	1	LSHB_STRCA	P80664 struthio ca
38	265	19.7	112	1	LSHB_RANCA	P80071 rana catesb
39	260	19.3	159	1	LSHB_MELGA	P45646 meleagris g
40	258	19.2	166	1	LSHB_COTUA	P43657 coturnix co
41	257	19.1	137	1	GTH2_ACALA	Q90225 acanthopagr
42	255	18.9	139	1	GTH2_MORSA	Q91121 morone saxa
43	255	18.9	146	1	GTH2_TRITC	Q9PW98 trichogaste
44	254	18.9	138	1	LSHB_CANFA	P54828 canis fami
45	253	18.8	127	1	GTH1_ANGUA	Q9Y9K3 anguilla ja

ALIGNMENTS

RESULT 1
ID CGHB_HUMAN STANDARD; PRT; 165 AA.
AC P01233; Q14000; Q13991;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Choriogonadotropin beta chain precursor (Chorionic gonadotropin beta subunit) (CG-beta).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=81012134; PubMed=6774259;
RA Fiddes J.C., Goodman H.M.;
RT "The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution of a gene by readthrough into the 3'-untranslated region.";
RT Nature 286:684-687(1980).
RN [2]
RP MEDLINE=84093590; PubMed=6690982;
RA Talmadge K., Yamvakopoulos N.C., Fiddes J.C.;
RT "Evolution of the genes for the beta subunits of human chorionic gonadotropin and luteinizing hormone.";
RT Nature 307:37-40(1984).
RN [3]
RP MEDLINE=84008141; PubMed=6194155;
RA Policastro P., Ovitl C.E., Hoshina M., Fukuoaka H., Boothby M.R., Bolme I.;
RT "The beta subunit of human chorionic gonadotropin is encoded by multiple genes.";
RT J. Biol. Chem. 256:11492-11499(1983).
RN [4]
RP MEDLINE=8117268; PubMed=7462224;
RA Birken S., Fetherston J., Canfield R.E., Bolme I.;
RT "The amino acid sequences of the prepeptides contained in the alpha and beta subunits of human chorionic gonadotropin.";
RT J. Biol. Chem. 256:1816-1823(1981).
RN [5]
RP MEDLINE=75211304; PubMed=1150658;
RA Morgan F.J., Birken S., Canfield R.E.;
RT "The amino acid sequence of human chorionic gonadotropin. The alpha subunit and beta subunit.";
RT J. Biol. Chem. 250:5247-5258(1975).
RN [6]
RP MEDLINE=74011267; PubMed=4795659;
RA Carlsen R.B., Bahn O.P., Swaminathan N.;
RT "Human chorionic gonadotropin. Linear amino acid sequence of the beta

RT subunit.";
 RL J. Biol. Chem. 248:6810-6827(1973).
 RN [7]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE=86195987; Pubmed=2422163;
 RA Policastro P.F., Daniels-McQueen S., Carle G., Bolme I.;
 RT "A map of the hcg beta-LH beta gene cluster.";
 RL J. Mol. Chem. 261:5907-5916(1986).
 RN [8]
 RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
 RX MEDLINE=81215630; Pubmed=7240231;
 RA Wise T., Bahl O.P.;
 RT "Assignment of disulfide bonds in the beta subunit of human chorionic gonadotropin.";
 RL J. Biol. Chem. 256:6587-6592(1981).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=90094415; Pubmed=1688430;
 RA Saccuzo Beebe J., Mountjoy K., Krzesicki R.F., Perini F.,
 RA Ruddon R.W.;
 RT "Role of disulfide bond formation in the folding of human chorionic gonadotropin beta subunit into an alpha beta dimer assembly-competent form.";
 RL J. Biol. Chem. 265:312-317(1990).
 RN [10]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=92314469; Pubmed=1820200;
 RA Weissnar G., Hiyama J., Renwick A.G.C.;
 RT "Site-specific N-glycosylation of human chorionic gonadotropin -- structural analysis of glycopeptides by one- and two-dimensional 1H NMR spectroscopy.";
 RL Glycobiology 1:393-404(1991).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=94261179; Pubmed=8202136;
 RA Laphorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,
 RA Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;
 RT "Crystal structure of human chorionic gonadotropin.";
 RL Nature 369:455-461(1994).
 CC -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -1- TISSUE SPECIFICITY: PLACENTA.
 CC -1- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
 CC -1- PHARMACEUTICAL: Available under the names Novarel (Pferring) and Profasi (Serono).
 CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: J00117; AAA96690.1; -;
 DR EMBL: X00265; CAA25068.1; ALT_INIT;
 DR EMBL: X00266; CAA25069.1; ALT_INIT;
 DR EMBL: M13504; AAA52005.1; -;
 DR EMBL: M13505; AAA52008.1; -;
 DR EMBL: M13503; AAA52009.1; -;
 DR EMBL: K03189; AAA53288.1; -;
 DR EMBL: K03187; AAA53288.1; JOINED.
 DR EMBL: K03188; AAA53288.1; JOINED.
 DR EMBL: K03183; AAA53287.1; -;
 DR EMBL: K00092; AAA53287.1; JOINED.
 DR EMBL: K03182; AAA53287.1; JOINED.
 DR PIR: A01502; KTHUB.
 DR PDB: 1HCN; 30-SEP-94.

DR PDB: 1HRP; 01-NOV-94.
 DR PDB: 1XUL; 15-MAY-97.
 DR GlycoSiteDB: P01233; -;
 DR Genew: HGNC:1886; CGB.
 DR Genew: HGNC:16451; CGB7.
 DR Genew: HGNC:16452; CGB5.
 DR MIM: 118860; -;
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR01545; Gly_hormoneb.
 DR Pfam: Pf00007; Cys_knot; 1.
 DR PRINTS: PR00438; GRCYSKNOT.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
 DR Hormone; Glycoprotein; Signal; Pharmaceutical; 3D-structure.
 KW SIGNAL
 FT 1
 FT CHAIN
 FT 21 165
 FT DISULFID 29 77
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT DISULFID 54 108
 FT DISULFID 58 110
 FT DISULFID 113 120
 FT CARBOHYD 33 33
 FT CARBOHYD 50 50
 FT CARBOHYD 141 141
 FT CARBOHYD 147 147
 FT CARBOHYD 152 152
 FT CARBOHYD 158 158
 FT VARIANT 137 137
 FT
 FT CONFLICT 24 24
 FT SEQUENCE 165 AA; 17739 MW; 5598FB9E51A05748 CRC04;
 SO
 Query Match 58.9%; Score 793; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 4.5e-59;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 101 KEPLRPGRPTNATLAEKEGCPVITVNTTICAGCYPTMTVLQGVLPALPOVVCYRD 160
 Db 22 KEPLRPGRPTNATLAEKEGCPVITVNTTICAGCYPTMTVLQGVLPALPOVVCYRD 81
 Oy 161 VRESIRLPGRPVNVSYAVALSCOCALCRSTDCGPKXPHLTCDPPRQDSSSS 220
 Db 82 VRESIRLPGRPVNVSYAVALSCOCALCRSTTDCGPKDHPLTCDPPRQDSSSS 141
 Oy 221 KAPPSLPSRLPGPSDTPILPQ 244
 Db 142 KAPPSLPSRLPGPSDTPILPQ 165
 RESULT 2
 CGB_PAPAN . STANDARD; PRT; 165 AA.
 ID CGB_PAPAN . PRT; 165 AA.
 AC P07434;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Choriongonadotropin beta chain precursor (Chorionic gonadotropin beta subunit) (CG-beta).
 GN CGB.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87106851; Pubmed=2433190;
 RA Crawford R.J., Tregear G.W., Niall H.D.;

```

RT "the nucleotide sequences of baboon chorionic gonadotropin
RL beta-subunit genes have diverged from the human."
CC -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- TISSUE SPECIFICITY: PLACENTA.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES
CC AND AT LEAST TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: M14966; AAA35383.1; -.
DR PIR: A25808; KTBAB.
DR HSSP: P01233; IXUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001545; Gly_hormoneB.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00068; GH; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone; Glycoprotein; Signal.
KW SIGNAL
FT 1 20 BY SIMILARITY.
FT CHAIN 21 165 CHORIOGONADOTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 141 141 O-LINKED (BY SIMILARITY).
FT CARBOHYD 147 147 O-LINKED (BY SIMILARITY).
FT CARBOHYD 152 152 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 165 AA; 17592 MW; 36D3E207A9F1E1C3 CRC64;

Query Match 48.3%; Score 651; DB 1; Length 165;
Best Local Similarity 79.2%; Pred. No. 2,7e-47;
Matches 118; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

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DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LH-
DE beta) (LH-B) (LH-B).
GN LHB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093590; PubMed=6690982;
RT Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT "Evolution of the genes for the beta subunits of human chorionic
RT gonadotropin and luteinizing hormone."
RT Nature 307:37-40(1984).
RN [2]
RP SEQUENCE OF 21-141.
RX MEDLINE=76062547; PubMed=1191677;
RT Saitam M.R., Li C.H.;
RT "Human pituitary lutropin. Isolation, properties, and the complete
RT amino acid sequence of the beta-subunit."
RT Biochim. Biophys. Acta 412:70-81(1975).
RN [3]
RP PRELIMINARY SEQUENCE OF 21-141.
RX MEDLINE=73090987; PubMed=4685398;
RT Shome B., Parlow A.F.;
RT "The primary structure of the hormone-specific, beta subunit of human
RT pituitary luteinizing hormone (hLH)."
RT J. Clin. Endocrinol. Metab. 36:618-621(1973).
RN [4]
RP PRELIMINARY PARTIAL SEQUENCE.
RX MEDLINE=73221227; PubMed=4719207;
RT Closset J., Hennen G., Leguin R.M.;
RT "Human luteinizing hormone. The amino acid sequence of the
RT subunit."
RT FEBS Lett. 29:97-100(1973).
RN [5]
RP STRUCTURE OF CARBOHYDRATE.
RX MEDLINE=91122088; PubMed=1991473;
RT Weishaar G., Hiyama J., Renwick A.G.C., Nimtz M.;
RT "NMR investigations of the N-linked oligosaccharides at individual
RT glycosylation sites of human lutropin."
RT Eur. J. Biochem. 195:257-268(1991).
RN [6]
RP STRUCTURE BY NMR OF 58-77.
RX MEDLINE=92357029; PubMed=1495492;
RT Keutmann H.T., Hsu Q.-X., Weiss M.A.;
RT "Structure of a receptor-binding fragment from human luteinizing
RT hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
RT resonance spectroscopy."
RT Mol. Endocrinol. 6:904-913(1992).
RN [7]
RP VARIANT ARG-74.
RX MEDLINE=92085985; PubMed=1727547;
RT Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
RT Jamason J.L.;
RT "Hypogonadism caused by a single amino acid substitution in the beta
RT subunit of luteinizing hormone."
RT New Engl. J. Med. 326:179-183(1992).
RN [8]
RP FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- TISSUE SPECIFICITY: PITUITARY.
CC -1- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: X00264; CAA25067.1; "-"
DR EMBL: S71273; AAD14960.1; ALT_SEQ.
DR PIR: A01497; UTHUB.
DR HSRP: P01233; 1XUL.
DR GlycoSuiteDB: P01229; -.
DR Genew: HGNC:6584; LHB.
DR MIM: 152780; -.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GE_cysknot.
DR InterPro: IPR001545; Gly_hormoneb.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PRU0438; GFCYSKNOT.
DR SMART: SMO0068; GHb; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal; Pseudohemaphroditism;
  Disease mutation.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAG. . .).
  /FTID-CAR_000045.
FT VARIANT 74 74 O -> R (IN HYPOGONADISM; LACK OF
  RECEPTOR-BINDING).
  /FTID-VAR_003189.
FT CONFLICT 39 39 E -> Q (IN REF. 2).
FT CONFLICT 76 76 MISSING (IN REF. 2).
FT CONFLICT 132 135 HPOL -> POH (IN REF. 2).
SQ SEQUENCE 141 AA; 15345 MW; EA11766253113F7C CAC64;

Query Match 40.1%; Score 540; DB 1; Length 141;
Best Local Similarity 85.0%; Pred. No. 3.7e-38;
Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 101 KEPLARRRCRPINATLAVKEGCPVCITYNTTICAGYCTPMTRVLOGVLPALPQVVCNRRD 160
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 22 REPLRPWPHINAIILAVKEGCPVCITYNTTICAGYCTPMTRVLOGVLPALPQVVCYTRD 81

QY 161 VFESIRLPGCRPGVNPVSVAVALSCCALCRSTTSCGGGKHPLRCDPR 213
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 82 VAFESIRLPGCRPGVNPVSVAVALSCCALCRSTTSCGGGKHPLRCDPR 134

RESULT 4
CGHB_CALJA STANDARD: PRT: 164 AA.
NC P51500;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Choriongonadotropin beta chain precursor (Chorionic gonadotropin beta
  subunit) (CG-beta).
DE CGB.
OS Callithrix jacchus (Common marmoset).
OC Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callithrix.
OX NCBI_TaxID=9483;
RX MEDLINE=96115012; PubMed=7492691;
RA Stimula A.P., Amato F., Faest R., Lopata A., Berka J., Norman R.J.;
  "Luteinizing hormone/chorionic gonadotropin bioactivity in the common

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RT	matmoset (Callitrix jacchus) is due to a chorionic gonadotropin molecule with a structure intermediate between human chorionic gonadotropin and human luteinizing hormone.";
RL	Biol. Reprod. 53:380-389(1995).
CC	-1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC	-1- SUBUNIT: HETEROIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONTERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC	-1- TISSUE SPECIFICITY: PLACENTA.
CC	-1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
CC	-----
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CC	-----
DR	EMBL; U04447; AAC00029.1; .
DR	HSSP; P01233; 1XU.
DR	InterPro; IPR0000359; Cys_knot.
DR	InterPro; IPR002400; GF_cysknot.
DR	InterPro; IPR001545; Gly_hormoneb.
DR	Pfam; PF00007; Cys_Knot; 1.
DR	PRINTS; PR00438; GF_CYSKNOT.
DR	SMART; SM00068; GHb; 1.
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW	Hormone; Glycoprotein; Signal.
FT	SIGNAL 1 20 BY SIMILARITY.
FT	CHAIN 21 164 CHORIOGONADOTROPIN BETA CHAIN.
FT	DISULFID 29 77 BY SIMILARITY.
FT	DISULFID 43 92 BY SIMILARITY.
FT	DISULFID 46 130 BY SIMILARITY.
FT	DISULFID 54 108 BY SIMILARITY.
FT	DISULFID 58 110 BY SIMILARITY.
FT	DISULFID 113 120 BY SIMILARITY.
FT	CARBOHYD 50 50 N-LINKED (GLCNAG. . .) (BY SIMILARITY).
FT	CARBOHYD 146 146 N-LINKED (GLCNAG. . .) (BY SIMILARITY).
SO	SEQUENCE 164 AA; 17712 MW; 0CD92DDC2618FA6 CRC64;
Query Match	38.3%; Score 516.5; DB 1; Length 164;
Best Local Similarity	66.0%; Pred. No. 3.9e-36;
Matches 95; Conservative 17; Mismatches 31; Indels 1; Gaps 1;	
OY	101 KEPLRRCRPINATLAVEREGCPVCITVNTTCAGYCPTMRVLQGVLPALPQVCYNRD 160 : : :
DB	22 KEPLRPLCRPNVALIAAEKEGPCVAENTTTICAGCYCSMVRVLTQIIPLPQSCYNHE 81 : : :
OY	161 VRFESIRLRPGCGRGVNPVSAVALSCCALCRSTTPCGGCKHDPLLCDPDRPDSSSS 220 ::: : :: : :
DB	82 LRFVSIVRLPGGRPGVDVPASMPALSCRCGLCRRSYSCGSLRNELPCDYTFOD-SSS 140 ::: : :: : :
OY	221 KAPPSPSPRLPGPSDTPILPQ 244 : :
DB	141 KDPRNLTPSQLEPPADPLVPQ 164 : :
RESULT 5	
LSHB_EOUBU	
ID	LSHB_EOUBU STANDARD; PRT; 169 AA.
AC	O46641;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DE	15-JUN-2002 (Rel. 41, last annotation update)
DE	lutropin/choriogonadotropin beta chain precursor (LSH-B/Cg-B)
DE	(luteinizing hormone beta subunit).
LN	Lhb.
OS	Equus burchelli (Plains zebra) (Equus quagga).

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactylia; Equidae; Equus.  
XX NCBI_TaxID=9790;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=pituitary; PubMed=10341734;  
RA MEDLINE=99273280; Pubmed=10341734;  
RX Choppineau M., Martinat N., Pourchet C., Stewart F., Combarnous Y.,  
RA Guillon F.;  
RT "Cloning, sequencing and functional expression of zebra (Equus  
burchelli) LH";  
RL J. Reprod. Fert. 115:159-166(1999).  
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
CC FAMILY.  
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CC -----  
DR EMBL: Y16265; CAA76146.1; -  
DR HSP: P01233; 1XU.  
DR InterPro: IPR000359; Cys_knot.  
DR InterPro: IPR002400; GF_cysknot.  
DR InterPro: IPR001545; Gly_hormoneb.  
DR Pfam: PF00007; Cys_knot; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR SMART: SM00068; GHb; 1.  
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.  
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.  
KW Hormone; Glycoprotein; Signal.  
FT SIGNAL 1 20 BY SIMILARITY.  
FT CHAIN 1 169 LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.  
FT DISULFID 29 77 BY SIMILARITY.  
FT DISULFID 43 92 BY SIMILARITY.  
FT DISULFID 46 130 BY SIMILARITY.  
FT DISULFID 54 108 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 113 120 BY SIMILARITY.  
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 169 AA; 17824 MW; 322DF24AEAA93E9 CRC64;  
Query Match 35.2%; Score 474; DB 1; Length 169;  
Best Local Similarity 60.5%; Pred. No. 1.4e-32;  
Matches 89; Conservative 16; Mismatches 32; Indels 10; Gaps 3;  
QY 103 PLRPRCPINATLAVEKGCPCVITVNTTICAGYCPMTFRLVGLPALPQVYCNVDR 162  
DB 24 PLRPLCRPINATLAKEKACPICITFTTICAGYCPMSVWVMPALPPIQVCTYREL 83  
QY 163 FESIRLPGCPGPNVYVAVALSCQCALCRSTTDCGPRDHLPTCDPRQDSSSKA 222  
DB 84 FASIRLPGCPGPNVYVAVALSCQCALCRSTTDCGPRDHLPTCDPRQDSSSKMD 140  
QY 223 PP--PSLPSRLPGSDPTPLPQTS 247  
DB 141 PPSQPLMTSTSTPTFGASN-----RSSH 162  
RESULT 6  
LSHB_EQUUS STANDARD; PRT; 169 AA.  
AC P19794;  
DT 01-FEB-1991 (Rel. 17, Created)
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DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE lutropin/choriogonadotropin beta chain precursor (LSH-B/GS-B)  
DE (lutensizing hormone beta subunit).  
GN LHB.  
OS Equus asinus (Donkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactylia; Equidae; Equus.  
XX NCBI_TaxID=9793;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Choppineau M., Combarnous Y., Allen W.R., Stewart F.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP PRELIMINARY SEQUENCE OF 105-169 FROM N.A.  
RC TISSUE=placenta;  
RX MEDLINE=90262634; Pubmed=2344391;  
RA Leigh S.E.A., Stewart F.;  
RT "Partial cDNA sequence for the donkey chorionic gonadotropin-beta  
RT subunit suggests evolution from an ancestral LH-beta gene.";  
RL J. Mol. Endocrinol. 4:143-150(1990).  
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
CC FAMILY.  
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CC -----  
DR EMBL: X80116; CAA56422.1; -  
DR EMBL: X53669; CAA37709.1; ALF_SEQ.  
DR PIR: S15676; S15676.  
DR HSP: P01233; 1XU.  
DR InterPro: IPR000359; Cys_knot.  
DR InterPro: IPR002400; GF_cysknot.  
DR InterPro: IPR001545; Gly_hormoneb.  
DR Pfam: PF00007; Cys_knot; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR SMART: SM00068; GHb; 1.  
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.  
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.  
KW Hormone; Glycoprotein; Signal.  
FT SIGNAL 1 20 BY SIMILARITY.  
FT CHAIN 1 169 LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.  
FT DISULFID 29 77 BY SIMILARITY.  
FT DISULFID 43 92 BY SIMILARITY.  
FT DISULFID 46 130 BY SIMILARITY.  
FT DISULFID 54 108 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 113 120 BY SIMILARITY.  
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (PROBABLE).  
SQ SEQUENCE 169 AA; 17943 MW; AED20891B56FA7C CRC64;  
Query Match 34.1%; Score 459; DB 1; Length 169;  
Best Local Similarity 57.9%; Pred. No. 2.4e-31;  
Matches 84; Conservative 15; Mismatches 38; Indels 8; Gaps 1;  
QY 103 PLRPRCPINATLAVEKGCPCVITVNTTICAGYCPMTFRLVGLPALPQVYCNVDR 162  
DB 24 PLRPLCRPINATLAKEKACPICITFTTICAGYCPMSVWVMPALPPIQVCTYREL 83  
QY 163 FESIRLPGCPGPNVYVAVALSCQCALCRSTTDCGPRDHLPTCDPRQDSSSKA 222  
DB 84 FASIRLPGCPGPNVYVAVALSCQCALCRSTTDCGPRDHLPTCDPRQDSSSKADPS 143
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FT CHAIN 20 144 ALPHA-1 MATING PHEROMONE.
FT PEPTIDE 90 102 MATING FACTOR ALPHA (1ST COPY).
FT PEPTIDE 111 123 MATING FACTOR ALPHA (2ND COPY).
FT PEPTIDE 132 144 MATING FACTOR ALPHA (3RD COPY).
SQ SEQUENCE 144 AA; 16091 MW; 9783C2B8AA98F996 CRC64;

Query Match 31.9%; Score 429.5; DB 1; Length 144;
Best Local Similarity 83.5%; Pred. No. 5,6e-29;
Matches 91; Conservative 6; Mismatches 5; Indels 7; Gaps 2;

QY 1 MRPSIFTVLFAASSALAAPVNTTDETAQIPAEAVIGYSDLEGGDFVAVLPFSNSTN 60
DB 1 MRPSIFTVLFAASSALAAPVNTTDETAQIPAEAVIGYLDLEGGDFVAVLPFSNSTN 60

QY 61 NGLLFINTTIASTAAKEGVSLEKREA--YVEFDGCGDKLEPLRPR 107
DB 61 NGLLFINTTIASTAAKEGVSLEKREA--YVEFDGCGDKLEPLRPR 104

RESULT 12
MFA3_YEAST STANDARD; PRT; 165 AA.
AC P01149;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mating factor alpha-1 precursor (Alpha-1 mating pheromone) [Contains:
DE Mating factor alpha1].
GN MFA1 OR MF-ALPHA-1 OR YPL187W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=83246532; PubMed=6306574;
RA Singh A., Chen E.Y., Lugovoy J.M., Chang C.N., Hitzeman R.A.,
RA Seeburg P.H.;
RA "Saccharomyces cerevisiae contains two discrete genes coding for the
RT alpha-factor pheromone."
RL Nucleic Acids Res. 11:4049-4063(1983).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=83050979; PubMed=6754095;
RA Kurjan J., Herskowitz I.;
RA "Structure of a yeast pheromone gene (MF alpha): a putative
RT alpha-factor precursor contains four tandem copies of mature
RT alpha-factor."
RL Cell 30:933-943(1982).
RN 13
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoorge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., Dipolo T., Dubois E., Duescherhoef A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA Hunke-Smith S., Hyman R., Johnston M., Kalman S., Klein K.,
RA Komp C., Kurd O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marthe R., Messenguy F., Mewes H.-W., Mitrifati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA Scherens B., Schram S., Schroeder M., Sidu A.M., Teteilin H.,
RA Uristesazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA Zhong W.W., Zollner A., Vo D.H., Han J.;
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."
RT Nature 387:103-105(1997).
RN 14
RP SEQUENCE OF 1-9 FROM N.A.

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RX MEDLINE=88038871; PubMed=2959859;
RA Inokuchi K., Nakayama A., Hishinuma F.;
RT "Identification of sequence elements that confer cell-type-specific
RT control of MF alpha 1 expression in Saccharomyces cerevisiae."
RL Mol. Cell. Biol. 7:3185-3193(1987).
RN 15
RP SEQUENCE OF THE ACTIVE FACTOR.
RA Stoezler D., Kiltz H.-H., Duntze W.;
RT "Primary structure of alpha-factor peptides from Saccharomyces
RT cerevisiae."
RL Eur. J. Biochem. 69:397-400(1976).
RN 16
RP SEQUENCE OF THE ACTIVE FACTOR.
RX MEDLINE=78087498; PubMed=340452;
RA Tanaka T., Kita H., Murakami T., Narita K.;
RT "Purification and amino acid sequence of mating factor from
RT Saccharomyces cerevisiae."
RL J. Biochem. 82:1681-1687(1977).
CC -1- FUNCTION: THE ACTIVE FACTOR IS EXCRETED INTO THE CULTURE MEDIUM BY
CC HAPLOID CELLS OF THE ALPHA MATING TYPE AND ACTS ON CELLS OF THE
CC OPPOSITE MATING TYPE (TYPE A). IT MEDIATES THE CONJUGATION PROCESS
CC BETWEEN THE TWO TYPES BY INHIBITING THE INITIATION OF DNA
CC SYNTHESIS IN TYPE A CELLS AND SYNCHRONIZING THEM WITH TYPE ALPHA.
CC -1- SIMILARITY: THE MATING FACTOR ALPHA-1 PRECURSOR IS IDENTICAL IN
CC S.ITALICUS, S.UVAKUM AND S.CEREVISIAE, EXCEPT FOR THE NUMBER OF
CC TANDEM REPEAT UNITS: 5, 3 AND 4 RESPECTIVELY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01581; CAA25734.1; -
DR EMBL; X01581; CAA25735.1; ALT_SEQ.
DR EMBL; X01581; CAA25736.1; ALT_SEQ.
DR EMBL; X01581; CAA25737.1; ALT_SEQ.
DR EMBL; X01581; CAA25738.1; ALT_SEQ.
DR EMBL; J01340; AAA88727.1; -
DR EMBL; Z73543; CAA97899.1; -
DR EMBL; M17301; AAA34777.1; -
DR EMBL; A14990; CAA01206.1; -
DR PIR; A01413; JFBI1.
DR SCD; S0006108; MF(ALPHA)1.
KW Pheromone; Cleavage on pair of basic residues; Repeat; Signal.
KW SIGNAL
FT CHAIN 1 19 OR 20 (PROBABILE).
FT PEPTIDE 20 165 ALPHA-1 MATING PHEROMONE.
FT PEPTIDE 90 102 MATING FACTOR ALPHA (1ST COPY).
FT PEPTIDE 111 123 MATING FACTOR ALPHA (2ND COPY).
FT PEPTIDE 132 144 MATING FACTOR ALPHA (3RD COPY).
FT PEPTIDE 153 165 MATING FACTOR ALPHA (4TH COPY).
FT CONFLICT 42 42 L -> S (IN REF. 2).
SQ SEQUENCE 165 AA; 18642 MW; 826ACB932DE3D128 CRC64;

Query Match 31.9%; Score 429.5; DB 1; Length 165;
Best Local Similarity 83.5%; Pred. No. 5,6e-29;
Matches 91; Conservative 6; Mismatches 5; Indels 7; Gaps 2;

QY 1 MRPSIFTVLFAASSALAAPVNTTDETAQIPAEAVIGYSDLEGGDFVAVLPFSNSTN 60
DB 1 MRPSIFTVLFAASSALAAPVNTTDETAQIPAEAVIGYLDLEGGDFVAVLPFSNSTN 60

QY 61 NGLLFINTTIASTAAKEGVSLEKREA--YVEFDGCGDKLEPLRPR 107
DB 61 NGLLFINTTIASTAAKEGVSLEKREA--YVEFDGCGDKLEPLRPR 104

RESULT 13
MFA1_YEAST STANDARD; PRT; 186 AA.
AC P25041;

```

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DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mating factor alpha precursor (Alpha mating pheromone).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Italcus / IFO 0253;
RA MEDLINE=88194702; Pubmed=2834101;
RX Kilda K., Hishinuma F.;
RT "Evidence for preferential multiplication of the internal unit in
RT tandem repeats of the mating factor alpha genes in Saccharomyces
RT yeasts."
RL Curr. Genet. 13:1-5(1988).
CC -1- FUNCTION: THE ACTIVE FACTOR IS EXCRETED INTO THE CULTURE MEDIUM BY
CC HAPLOID CELLS OF THE ALPHA MATING TYPE AND ACTS ON CELLS OF THE
CC OPPOSITE MATING TYPE (TYPE A). IT MEDIATES THE CONUGATION PROCESS
CC BETWEEN THE TWO TYPES BY INHIBITING THE INITIATION OF DNA
CC SYNTHESIS IN TYPE A CELLS AND SYNCHRONIZING THEM WITH TYPE ALPHA.
CC -1- SIMILARITY: THE MATING FACTOR ALPHA-1 PRECURSOR IS IDENTICAL IN
CC S. ITALICUS, S. UVARUM AND S. CEREVISIAE, EXCEPT FOR THE NUMBER OF
CC TANDEM REPEAT UNITS: 5, 3 AND 4 RESPECTIVELY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: M55016; AAA34778.1; -
KW Pheromone; Cleavage on pair of basic residues; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 186
FT PEPTIDE 90 102 ALPHA-1 MATING PHEROMONE.
FT PEPTIDE 111 123 MATING FACTOR ALPHA (1ST COPY).
FT PEPTIDE 132 144 MATING FACTOR ALPHA (2ND COPY).
FT PEPTIDE 153 165 MATING FACTOR ALPHA (3RD COPY).
FT PEPTIDE 174 186 MATING FACTOR ALPHA (4TH COPY).
SQ SEQUENCE 186 AA; 21165 MW; 8F014F9EB263BDCF CRC64;

Query Match 31.9%; Score 429.5; DB 1; Length 186;
Best Local Similarity 83.5%; Pred. No. 7.6e-29;
Matches 91; Conservative 6; Mismatches 5; Indels 7; Gaps 2;

QY 1 MRPSFTAVLPAASSALAPVTTTDEDAQIPAEAVITGYSDLEGDFVAVLPFSNSTN 60
DB 1 MRPSFTAVLPAASSALAPVTTTDEDAQIPAEAVITGYDLEGDFVAVLPFSNSTN 60
QY 61 NGLFINTTIASTAKEEGVSLKREAEV--YVEPDGCKDEKLEPR 107
DB 61 NGLFINTTIASTAKEEGVSLKREAEV--YVEPDGCKDEKLEPR 104
DB 61 NGLFINTTIASTAKEEGVSLKREAEV--YVEPDGCKDEKLEPR 104

RESULT 14
LSHB_CERSI
ID LSHB_CERSI STANDARD: PRT: 141 AA.
AC 077835; 019102;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB1 AND LHB2.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_TaxID=9807;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=98389253; Pubmed=9723860;
RA Lund L.A., Sherman G.B.;
RT "Purification of the southern white rhinoceros (Ceratotherium simum
RT simum) luteinizing hormone beta subunit gene."
RL J. Mol. Endocrinol. 21:19-30(1998).
RN [2]
RP SEQUENCE OF 7-141 FROM N.A.
RC TISSUE=pituitary;
RX MEDLINE=97449288; Pubmed=9305757;
RA Sherman G.B., Lund L.A., Bunick D., Winn R.J.;
RT "Characterization and phylogenetic significance of rhinoceros
RT luteinizing hormone beta (LHbeta) subunit messenger RNA structure,
RT complementary DNA sequence and gene copy number."
RL Gene 195:131-139(1997).
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: AF024521; AAC36049.1; -
DR EMBL: AF024520; AAC36048.1; -
DR EMBL: U72659; AAB71983.1; -
DR HSSP: P01233; 1XUL.
DR Interpro: IPR000359; Cys_knot.
DR Interpro: IPR002400; GF_cysknot.
DR Interpro: IPR001545; Gly_hormoneb.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00068; GH1.1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141
FT DISULFID 29 77 LUTROPIN BETA CHAIN.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 22 22 R -> K (IN REF. 2).
SQ SEQUENCE 141 AA; 14930 MW; FFEDB157C51976C9 CRC64;

Query Match 31.6%; Score 426; DB 1; Length 141;
Best Local Similarity 67.3%; Pred. No. 1.1e-28;
Matches 74; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 103 PLRPRCPINATLAVEGEGPCVITVNTTTCAGCPTMTVLOGVLPALPOVVCNTRDVR 162
DB 24 PLRPLCRPINATLAVEGEGPCVITVNTTTCAGCPSMVVLPALPAPQVPCYTHELR 83
QY 163 FESIRLPGCPRGVNPVYVAVALSCOCALCRSTRTPDGKDPHLCDDP 212
DB 84 FASIRLPGCPRGVNPVYVAVALSCRCGRCRLSSDGGFRAOPLACDRP 133

RESULT 15
LSHB_PIG
ID LSHB_PIG STANDARD: PRT: 141 AA.
AC P01322;

```

DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
 beta) (LSH-B) (LH-B).
 GN LHB.
 CN Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91063934; PubMed=1701088;
 RA Ezashi T., Hirai T., Kato T., Wakabayashi K., Kato Y.;
 RT "The gene for the beta subunit of porcine LH: clusters of GC boxes
 and CACC elements";
 RL J. Mol. Endocrinol. 5:137-146(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89306142; PubMed=2744222;
 RA Kato Y., Hirai T.;
 RT "Cloning and DNA sequence analysis of the cDNA for the precursor of
 porcine luteinizing hormone (LH) beta subunit.";
 RL Mol. Cell. Endocrinol. 62:47-53(1989).
 RN [3]
 RP SEQUENCE OF 21-139.
 RX MEDLINE=74075724; PubMed=4770795;
 RA Maghain-Register G., Hennen G.;
 RT "Luteinizing hormone. The primary structures of the beta-subunit from
 bovine and porcine species.";
 RL Eur. J. Biochem. 39:235-253(1973).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CHAIN WHICH CONTERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 FAMILY.
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 CC -----
 DR EMBL, D00579; BAA0457.1; -.
 DR PIR, A30322; UTPGB.
 DR PIR, A48170; A48170.
 DR HSSP, P01233; 1XUL.
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR Pfam: PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KM Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 141
 FT DISULFID 29 77 LUTROPIN BETA CHAIN.
 FT DISULFID 43 92 BY SIMILARITY.
 FT DISULFID 46 130 BY SIMILARITY.
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120 BY SIMILARITY.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).
 FT MOD_RES 21 21 BLOCKED.
 FT VARIANT 30 30 R -> Z.
 FT VARIANT 40 40 N -> D (IN REF. 3).
 FT CONFLICT 62 62 V -> R (IN REF. 3).
 FT CONFLICT 62 62

FT CONFLICT 83 83 S -> I (IN REF. 3).
 FT CONFLICT 87 87 I -> S (IN REF. 3).
 FT CONFLICT 122 123 GP -> PG (IN REF. 3).
 SQ SEQUENCE 141 AA; 14889 MW; 803E8E7C59F3C2CF CRC64;

Query Match 31.6%; Score 425; DB 1; Length 141;

Best local Similarity 67.3%; Pred. No. 1,3e-28; Mismatches 26; Indels 0; Gaps 0;

QY 103 PLRRRCRPIATLAEKEGCPVCITVNTTTCAGYCPMTFRVLGGVLPALPQVVCNTRDYR 162
 Db 24 PLRRRCRPIATLAEKEGCPVCITVNTTTCAGYCPMTFRVLGGVLPALPQVVCNTRDYR 83
 QY 163 FESIRLPGCPRGVNPVYSVAVALSCCALCRSTTDCGGEKDHPLTCDDP 212
 Db 84 FASIRLPGCPRGVNPVYSVAVALSCCALCRSTTDCGGEKDHPLTCDDP 133

Search completed: November 20, 2002, 17:27:59
 Job time : 10.986 secs

GenCore version 5.1.3
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ow protein - protein search, using sw model

OM protein - protein search, using SW-MOL
November 20, 2002, 17:26:27 ; Search time 31.1339 Seconds
(without alignments)
Run on: 1667.815 Million cell updates/sec

US-09-787-494-4

Sequence:

Gapop 10.0 / 2015 306047115 residues

Number of hits satisfying chosen parameters:

Minimum	DB seq	length:	0
		length:	20000000000

Maximum DB seq length: 20000000

post-processing:	Minimum	Maximum
	Match	100%

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Database :
SPRMBRL.21:*
1:  sp.archae:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.organelle:*
9:  sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.bacteriap:*
16:
17: sp.archaeap:*
```

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	788	58.5	159	4	08RTT5	08rtt5 homo sapien
2	783	58.1	159	4	08WXL2	08wxl2 homo sapien
3	778	56.7	159	4	08WXL3	08wxl3 homo sapien
4	764	56.3	159	4	08WXL1	08wxl1 homo sapien
5	758	54.7	159	6	08WNC4	08wnc4 porngo pygma
6	737	54.6	157	6	08WNC7	08wnc7 porngo pygma
7	735	54.6	157	6	08WNC5	08wnc5 porngo pygma
8	735	54.6	157	6	08WNC6	08wnc6 porngo pygma
9	726	53.9	165	6	08BEH1	08beh1 macaca fasc
10	657	48.8	159	6	08WNB0	08wnb0 macaca mula
11	654	48.6	159	6	08WNB9	08wnb9 macaca fasc
12	653	48.5	165	6	08PEH2	08peh2 macaca fasc
13	652	48.4	159	6	08WNB2	08wnb2 colobus que
14	646	48.0	159	6	08WNB8	08wnb8 macaca mulata
15	646	48.0	159	6	08WNB1	08wnb1 colobus que
16	644	47.8	159	6	08WNB1	08wnb1 colobus que

17	642	47.7	165	6	09GL37	099p48 mus muscula
18	642	47.7	165	11	099p48	08wnb3 colobus que
19	631	46.8	159	6	08BNB3	08wnb3 colobus que
20	628	46.6	159	6	08BNB4	08wnb4 presbytis o
21	616	45.7	157	6	08BNB9	08wnb3 presbytis o
22	615	45.7	157	6	08BNB3	08wnb0 presbytis o
23	609	45.2	157	6	08BNB3	08wnb0 presbytis o
24	607	45.1	157	6	08BNB3	08wnb2 presbytis o
25	605	44.9	157	6	08BNB3	08wnb2 pongo pygma
26	574	42.6	136	6	08BNB8	08wx10 homo sapien
27	540	40.1	136	4	08BNB8	08wnb5 presbytis o
28	515	38.2	136	6	08BNB6	08wnb5 colobus que
29	505	37.5	136	6	08BNB5	08wnb5 actus trivi
30	498.5	37.0	136	6	08BNB6	08wnb7 macaca mula
31	498	37.0	136	6	08BNB7	08wnb7 macaca mula
32	476.5	35.4	156	6	08BNB7	08wnb7 calliobus
33	444	33.0	156	6	08BNB7	08wnb19 paltheera ti
34	441	32.7	152	6	099D19	08wnb5 tarsius ban
35	446	32.4	136	6	08BNB5	08wna5 galago sene
36	435	32.3	136	6	08BNB2	08wna2 daudentonia
37	432	32.1	136	6	08BNB4	08wna3 lemur varie
38	431	32.0	136	6	08BNB3	08wna0 cynocephali
39	431	32.0	139	6	08BNB3	08wnb2778 ractus nov
40	431	32.0	141	6	08BNB1	08wnb18 alluropoda
41	427	31.7	136	6	08BNB1	08wna9 loris tardi
42	413	30.7	136	6	08BNB9	08wn99 pteropus ly
43	411	30.5	86	3	002436	002436 saccharomyc
44	396	29.4	127	11	0924A6	0924A6 cavia porce
45	396	29.4	135	11	0924A7	0924A7 cavia porce

ALIGNMENTS

					RESULT	1
ID	O8WT75	PRELIMINARY:	PRT:	159 AA.		
AC	O8WT5					
Dt	01-MAR-2002 (TREMblrel.)	20,	Created)			
Dt	01-MAR-2002 (TREMblrel.)	20,	Last sequence update)			
Dt	01-JUN-2002 (TREMblrel.)	21,	Last annotation update)			
DE	Chorionic gonadotropin beta subunit (Fragment).					
GN	GCB.					
OS	Homo sapiens (Human) .					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[]					
RP	SOURCE FROM N.A.					
RA	Mason G.A., Ruvoilo M.; has a recent origin in primates and an					
RT	"Chorionic gonadotropin selection."					
RL	evolutionary history of selection.";					
EMBL:	(JUL-2001) to the EMBL/genbank/DBPJ databases.					
Submitted	AAL69705.1 ; -					
EMBL:	AF397560; AAL69708.1 ; -					
DR	EMBL; AF397560; GIY_knoc.					
DR	IPIR000359; GIY_hormoneB.					
DR	InterPro; IPR001545; Gly_hormoneB.					
DR	pfam; PF00007; Cys_knoc; 1.					
DR	SMART; SMD0068; GHF_1.					
DR	PROSITE; PS00261; GLXCO_HORMONE_BETA_1; UNKNOWN_1.					
DR	PROSITE; PS00261; GLXCO_HORMONE_BETA_2; UNKNOWN_1.					
FT	NON_TER	1				
FT	NON_TER	159				
SEQUENCE	AA: 159 AA: 16944 MM: 246BA938796A1727 CRC64:					
Query Match	Best Local Similarity	58.5%; Score 788; DB 4; Length 159;				
Matches 143;	Conservative	100.0% ; Pred. No. 2,1e-67;				
		Mismatches 0; Indels 0; Gaps				
QY	101 KEPLERCRPINATLAVERKCEPCIVNTTCICAGCPTMTFLVGLGVPALPÖVVNCYRD 160 +++++ KEPLERCRCPINATLAVERKCEPCIVNTTCICAGCTPTRNLGVLPALPÖVVNCYRD	76				
Db	17					

OY 161 VRFESIRLPGCGPGRVNPVSYAVALSCQALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
DB 77 VRFESIRLPGCGPGRVNPVSYAVALSCQALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
OY 221 KAPPSLSPSRRLPGSPDPIPLP 243
DB 137 KAPPSLSPSRRLPGSPDPIPLP 159

RESULT 2

O8MXL2
ID O8MXL2 PRELIMINARY: PRT: 159 AA.
AC O8MXL2: 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Choriolic gonadotropin beta subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A.; Ruvolo M.;
RT "Choriolic gonadotropin has a recent origin in primates and an
evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF397579; AAL69707.1; EMBL/GenBank/DBJ databases.
DR InterPro: IPR000359; Cys_knot.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 159
FT SEQUENCE 159 AA; 16960 MW; 24761E38796A1727 CRC64;

Query Match

Best Local Similarity 58.1%; Score 783; DB 4; Length 159;
Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 101 KEPLRRCRPIINATLAVEGECPCITVNTTICAGCPTMTRVLGCVLPALPOVVCNTRD 160
DB 17 KEPLRRCRPIINATLAVEGECPCITVNTTICAGCPTMTRVLGCVLPALPOVVCNTRD 160
OY 161 VRFESIRLPGCGPGRVNPVSYAVALSCQALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
DB 77 VRFESIRLPGCGPGRVNPVSYAVALSCQALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
OY 221 KAPPSLSPSRRLPGSPDPIPLP 243
DB 137 KAPPSLSPSRRLPGSPDPIPLP 159

RESULT 3

O8MXL3
ID O8MXL3 PRELIMINARY: PRT: 159 AA.
AC O8MXL3: 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Choriolic gonadotropin beta subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A.; Ruvolo M.;
RT "Choriolic gonadotropin has a recent origin in primates and an
evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF397579; AAL69707.1; EMBL/GenBank/DBJ databases.
DR InterPro: IPR000359; Cys_knot.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 159
FT SEQUENCE 159 AA; 16909 MW; A598A73CC9757EE CRC64;

RT evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF397578; AAL69706.1; -
DR InterPro: IPR000359; Cys_knot.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 159
FT SEQUENCE 159 AA; 17006 MW; AFDCAE2542EC084 CRC64;

Query Match

Best Local Similarity 57.6%; Score 776; DB 4; Length 159;
Matches 141; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 101 KEPLRRCRPIINATLAVEGECPCITVNTTICAGCPTMTRVLGCVLPALPOVVCNTRD 160
DB 17 KEPLRRCRPIINATLAVEGECPCITVNTTICAGCPTMTRVLGCVLPALPOVVCNTRD 160
OY 161 VRFESIRLPGCGPGRVNPVSYAVALSCQALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
DB 77 VRFESIRLPGCGPGRVNPVSYAVALSCQALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
OY 221 KAPPSLSPSRRLPGSPDPIPLP 243
DB 137 KAPPSLSPSRRLPGSPDPIPLP 159

RESULT 4

O8MXL4
ID O8MXL4 PRELIMINARY: PRT: 159 AA.
AC O8MXL4: 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Choriolic gonadotropin beta subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A.; Ruvolo M.;
RT "Choriolic gonadotropin has a recent origin in primates and an
evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF397576; AAL69704.1; -
DR InterPro: IPR000359; Cys_knot.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 159
FT SEQUENCE 159 AA; 16909 MW; A598A73CC9757EE CRC64;

Query Match

Best Local Similarity 56.7%; Score 764; DB 4; Length 159;
Matches 139; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 101 KEPLRRCRPIINATLAVEGECPCITVNTTICAGCPTMTRVLGCVLPALPOVVCNTRD 160
DB 17 KEPLRRCRPIINATLAVEGECPCITVNTTICAGCPTMTRVLGCVLPALPOVVCNTRD 160
OY 161 VRFESIRLPGCGPGRVNPVSYAVALSCQALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
DB 77 VRFESIRLPGCGPGRVNPVSYAVALSCQALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
OY 221 KAPPSLSPSRRLPGSPDPIPLP 243


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08MNC5
ID Q8MNC5 PRELIMINARY: PRT: 157 AA.
AC Q8MNC5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE Choriionic gonadotropin beta subunit (Fragment)
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_Taxid=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Mascon G.A., Ruvoilo M.;
RT "Choriionic gonadotropin has a recent origin in primates and an
RT Evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF397584; AAL69712.1; -
DR InterPro: IPR001545; Gly_knot.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
FT NON_TER 1 157
SQ SEQUENCE 157 AA; 17027 MW; 8317774EDF4BD4ED CRC64;

Query Match
Best local Similarity 95.0%; Score 735; DB 6; Length 157;
Matches 133; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 101 KEPLRRCPINATLAVEKGGPCVITVNTTTCAGCTPTMTVLQGVLPALPQVVCNRYD 160
DB 17 KEPLRRCPINATLAVEKGGPCVITVNTTTCAGCTPTMTVLQGVLPALPQVVCNRYD 76
QY 161 VFEESIRLPGCGRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPFRDSSSS 220
DB 77 VFEETIRLPGCGRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPFRDSSSS 136
QY 221 KAPPSLPSRLPGSDPT 240
DB 137 KAPPSLPSRLPGSDPT 156

RESULT 9
Q8MNC6
ID Q8MNC6 PRELIMINARY: PRT: 157 AA.
AC Q8MNC6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE Choriionic gonadotropin beta subunit (Fragment)
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_Taxid=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Mascon G.A., Ruvoilo M.;
RT "Choriionic gonadotropin has a recent origin in primates and an
RT Evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF397583; AAL69711.1; -
DR InterPro: IPR001545; Gly_knot.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
FT NON_TER 1 157
SQ SEQUENCE 157 AA; 17027 MW; 8317774EDF4BD4ED CRC64;

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FT NON_TER 157 157
SQ SEQUENCE 157 AA; 16868 MW; 97BD27A014E1D4EC CRC64;

Query Match
Best local Similarity 53.9%; Score 726; DB 6; Length 157;
Matches 132; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 101 KEPLRRCPINATLAVEKGGPCVITVNTTTCAGCTPTMTVLQGVLPALPQVVCNRYD 160
DB 17 KEPLRRCPINATLAVEKGGPCVITVNTTTCAGCTPTMTVLQGVLPALPQVVCNRYD 76
QY 161 VFEESIRLPGCGRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPFRDSSSS 220
DB 77 VFEETIRLPGCGRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPFRDSSSS 136
QY 221 KAPPSLPSRLPGSDPT 240
DB 137 KAPPSLPSRLPGSDPT 156

RESULT 10
Q9BEH1
ID Q9BEH1 PRELIMINARY: PRT: 165 AA.
AC Q9BEH1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE Choriionic gonadotropin beta subunit 2.
OS Macaca fascicularis (Cebus eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-EMBRONIC TROPHOBLAST;
RA Wilken J.A., Matsuno K., Lasley B.L., Bedows E.;
RT "A Comparison of Choriionic Gonadotropin Expression by Human and
RT Macaque Trophoblast Cells."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY026360; AAR08644.1; -
DR HSP: P01233; 1XUL.
DR InterPro: IPR001545; Gly_knot.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ SEQUENCE 165 AA; 17743 MW; 2F21566B48592471 CRC64;

Query Match
Best local Similarity 48.8%; Score 657; DB 6; Length 165;
Matches 120; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 96 GGRDKEPLRRCPINATLAVEKGGPCVITVNTTTCAGCTPTMTVLQGVLPALPQVVCNRYD 155
DB 17 GARASKEPLRRCPINATLAVEKGGPCVITVNTTTCAGCTPTMTVLQGVLPALPQVVCNRYD 76
QY 156 CNYRDVRESIRLPGCGRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPFRDSSSS 215
DB 77 CNYREVRESIRLPGCGRGVNPVSYAVALSOCALCRSTTDCGPKDHPPLTCDPFRDSSSS 136
QY 216 DSSSKKAPPSLPSRLPGSDPT 244
DB 137 ASSSSKAPPSLPSRLPGSDPT 165

RESULT 11
Q8MNB0
ID Q8MNB0 PRELIMINARY: PRT: 159 AA.
AC Q8MNB0;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

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DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Choriionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Choriionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397600; AAL69728.1; -
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR001545; Gly_hormoneb.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 159
FT SEQUENCE 159 AA; 16853 MW; 7B64051C2E863870 CRC64;
SQ
Query Match 48.6%; Score 654; DB 6; Length 159;
Best Local Similarity 81.1%; Pred. No. 1.3e-54;
Matches 120; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
OY 96 GCRDLKEPLRRCRPIINATLAVERGECVCTVTNTTTCAGCPTMTRVLOGVLPALPOVY 155
DB 12 GAQASREPLRLCPRIINATLAERKACPVCTVTNTTTCAGCPTMTRVLOGVLPVPOVY 71
OY 156 CNVRDVFESIRLPGCGPVGVVSVYAVALSQCQALCRSTTDCGGRKDPHLCDDPRFQ 215
DB 72 CNVRDVFESIRLPGCGPVGVVSVYAVALSQCQALCRSTTDCGGRKDPHLCDDPRFQ 131
OY 216 DSSSSKAPPSLPSPSRPLPGSDPTPLP 243
DB 132 ASSSSKDPSPSPSPSRPLPGSDPTPLP 159
RESULT 12
OQ8WNA9 PRELIMINARY; PRT; 159 AA.
AC OQ8WNA9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Choriionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Choriionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397601; AAL69729.1; -
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR001545; Gly_hormoneb.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 159
FT SEQUENCE 159 AA; 16915 MW; 9231691EDDD82863 CRC64;
SQ
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Query Match 48.5%; Score 653; DB 6; Length 159;
Best Local Similarity 80.4%; Pred. No. 1.6e-54;
Matches 119; Conservative 9; Mismatches 20; Indels 0; Gaps 0;
OY 96 GCRDLKEPLRRCRPIINATLAVERGECVCTVTNTTTCAGCPTMTRVLOGVLPALPOVY 155
DB 12 GAQASREPLRLCPRIINATLAERKACPVCTVTNTTTCAGCPTMTRVLOGVLPVPOVY 71
OY 156 CNVRDVFESIRLPGCGPVGVVSVYAVALSQCQALCRSTTDCGGRKDPHLCDDPRFQ 215
DB 72 CNVRDVFESIRLPGCGPVGVVSVYAVALSQCQALCRSTTDCGGRKDPHLCDDPRFQ 131
OY 216 DSSSSKAPPSLPSPSRPLPGSDPTPLP 243
DB 132 ASSSSKDPSPSPSPSRPLPGSDPTPLP 159
RESULT 13
OQ9BEH2 PRELIMINARY; PRT; 165 AA.
AC OQ9BEH2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Choriionic gonadotropin beta subunit 1.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-EMBRYONIC TROPHOBLAST;
RA Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
RT "A Comparison of Choriionic Gonadotropin Expression by Human and
Macaque Trophoblast Cells.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY026359; AAK08643.1; -
DR HSSP; P01233; 1XUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR001545; Gly_hormoneb.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
FT SEQUENCE 165 AA; 17711 MW; 280DF602157D9940 CRC64;
SQ
Query Match 48.4%; Score 652; DB 6; Length 165;
Best Local Similarity 79.9%; Pred. No. 2.1e-54;
Matches 119; Conservative 8; Mismatches 22; Indels 0; Gaps 0;
OY 96 GCRDLKEPLRRCRPIINATLAVERGECVCTVTNTTTCAGCPTMTRVLOGVLPALPOVY 155
DB 17 GAQASREPLRLCPRIINATLAERKACPVCTVTNTTTCAGCPTMTRVLOGVLPVPOVY 76
OY 156 CNVRDVFESIRLPGCGPVGVVSVYAVALSQCQALCRSTTDCGGRKDPHLCDDPRFQ 215
DB 77 CNVRDVFESIRLPGCGPVGVVSVYAVALSQCQALCRSTTDCGGRKDPHLCDDPRFQ 136
OY 216 DSSSSKAPPSLPSPSRPLPGSDPTPLP 244
DB 137 ASSSSKDPSPSPSPSRPLPGSDPTPLP 165
RESULT 14
OQ8WNB2 PRELIMINARY; PRT; 159 AA.
AC OQ8WNB2;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Choriionic gonadotropin beta subunit (Fragment).
GN CGB.
```

OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
NCBI_TaxID=33548;
[1]
RP SEQUENCE FROM N.A.
RA Mastom G.A., Ruvoio M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397598; AAL69726.1; -
DR InterPro: IPR000359; Cys_knot.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART; SM00068; GH1; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 1
FT 159 159
SQ SEQUENCE 159 AA; 16972 MW; 725BA76BC287660 CRC64;

Query Match 48.0%; Score 646; DB 6; Length 159;
Best Local Similarity 81.8%; Pred. No. 7.5e-54;
Matches 117; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

OY 101 KEPLRRCRPIATLAVEKEGCPVCTVNTTICAGYCPMTRVGLPALPQVVCNRYD 160
DB 17 REPLRLCRPIATLAVEKEGCPVCTVNTTICAGYCPMTRVGLPALPQVVCNRYD 76
OY 161 VFESIRLPGCGPVGVPVSVAVASCALCRSTTDCGPKDHLTCDDPRFQDSSS 220
DB 77 VFESIRLPGCGPVGVPVSVAVASCALCRSTTDCGPKDHLTCDDPRFQDSSS 136
OY 221 KAPPSLPSPSLRPGSDTPILP 243
DB 137 KAPPSLPSPSLRPGSDTPILP 159

RESULT 15
O8WNA8
ID O8WNA8 PRELIMINARY; PRT; 159 AA.
AC O8WNA8;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
OC Cercopithecoidea; Macaca.
NCBI_TaxID=9544;
[1]
RP SEQUENCE FROM N.A.
RA Mastom G.A., Ruvoio M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397602; AAL69730.1; -
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR001545; Gly_hormoneB.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART; SM00068; GH1; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 1
FT 159 159
SQ SEQUENCE 159 AA; 17032 MW; 726E29F7A27E5C04 CRC64;

Query Match 48.0%; Score 646; DB 6; Length 159;
Best Local Similarity 80.8%; Pred. No. 7.5e-54;
Matches 118; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

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DB 14 RASREPLRLCRPIATLAVEKEGCPVCTVNTTICAGYCPMTRVGLPALPQVVCN 73
OY 158 YRVPFESTRLPGCGPVGVPVSVAVASCALCRSTTDCGPKDHLTCDDPRFQDSS 217
DB 74 YRVPFESTRLPGCGPVGVPVSVAVASCALCRSTTDCGPKDHLTCDDPRFQDSS 133
OY 218 SSSKAPPSLPSPSLRPGSDTPILP 243
DB 134 SSSKAPPSLPSPSLRPGSDTPILP 159

Search completed: November 20, 2002, 17:28:59
Job time : 31.1329 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:21 ; Search time 38.1818 Seconds
(without alignments)
879.454 Million cell updates/sec

Title: US-09-787-494-4

Perfect score: 1347

Sequence: 1 MRPSIFTAVLFPAASALAA.....LPGPSDPITLPOTSHHHHHH 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1347	100.0	252	21	AAV57316
2	886.5	65.8	176	21	AAV57315
3	804	59.7	273	20	AAV43292
4	802	59.5	273	20	AAV43285
5	795	59.0	209	20	AAV43299
6	795	59.0	212	20	AAV43304
7	795	59.0	265	22	AAU04602
8	795	59.0	265	22	AAU04614
9	795	59.0	265	22	AAE04474
10	795	59.0	265	22	AAE04486

11	793	58.9	145	20	AAW93434	Human hCG beta-sub
12	793	58.9	145	20	AAW95520	Human chorionic go
13	793	58.9	145	21	AAW20558	Human chorionic go
14	793	58.9	145	22	AAU04619	Human chorionic go
15	793	58.9	145	22	AAE04491	Human chorionic go
16	793	58.9	145	22	AAU00709	Beta-subunit of hu
17	793	58.9	145	22	AAU01139	Human chorionic go
18	793	58.9	145	22	AAW71765	Beta-human chorion
19	793	58.9	145	22	AAW04121	Beta subunit of hu
20	793	58.9	145	23	AAW50776	Human chorionic go
21	793	58.9	145	23	AAW83014	Beta-human chorion
22	793	58.9	165	12	AAW15043	Human chorionic go
23	793	58.9	165	20	AAV05748	Human chorionic go
24	793	58.9	165	20	AAW95358	Human chorionic go
25	793	58.9	165	21	AAW15358	Human chorionic go
26	793	58.9	165	22	AAW49896	Human chorionic go
27	793	58.9	165	23	AAU96134	Human chorionic go
28	793	58.9	203	20	AAV43298	AAV43298
29	793	58.9	206	20	AAV43303	Human CG beta subu
30	791.5	58.8	212	20	AAV43278	Human beta-hCG pro
31	790	58.6	165	19	AAW47473	Human chorionic go
32	790	58.6	165	19	AAW33639	Human chorionic go
33	790	58.6	165	19	AAW33637	Human chorionic go
34	789	58.6	145	20	AAW95530	Human chorionic go
35	789	58.6	165	20	AAW95508	Glycoprotein hormo
36	789	58.6	181	22	AAU04613	Gonadotropin analo
37	789	58.6	144	22	AAE04485	Human single chain
38	788.5	58.5	144	12	AAW15178	hCG histidine subs
39	788	58.5	145	12	AAW15171	hCG methionine sub
40	788	58.5	145	12	AAW15173	hCG histidine subs
41	788	58.5	165	20	AAW95514	Glycoprotein hormo
42	788	58.5	165	20	AAW95507	Glycoprotein hormo
43	788	58.5	165	20	AAW95509	hCG methionine sub
44	787	58.4	145	12	AAW15169	Human chorionic sub
45	787	58.4	145	14	AAW30939	Human chorionic go

ALIGNMENTS

RESULT 1	AAV57316	standard; Protein; 252 AA.
ID	AAV57316	
AC	AAV57316;	
XX		
DT	19-JUN-2000	(first entry)
XX		
DE	Alpha-mating factor fragment/betahCG fusion protein.	
XX		
KW	Human chorionic gonadotropin; hCG; betahCG; vaccine; chitosan;	
KW	infertility; betahCG/beta-gal; fusion protein.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200015253-A1.	
XX		
PD	23-MAR-2000.	
XX		
PF	16-SEP-1999;	99NO-US21591.
XX		
PR	17-SEP-1998;	98US-0100766.
XX		
PA	(ZONA-) ZONAGEN INC.	
PI	Harris J, Martinez M;	
XX		
DR	WPI; 2000-271258/23.	
XX		
DR	N-PSDB; AA290610.	
XX		
PT	Novel human beta-subunit chorionic gonadotropin vaccines used to	
PT	interrupt fertility in mammals by the immunological inactivation of the	
PT	pregnancy hormone chorionic gonadotropin	

XX Claim 5: Page 34-35; 39pp; English.

CC The invention provides novel vaccine compositions which comprise the
CC beta-subunit of human chorionic gonadotropin (betahCG) in combination
CC with chitosan-based adjuvants. The vaccines are used to induce
CC infertility especially transient infertility, in female mammals. The
CC compositions are also used for antibody production. The vaccines comprise
CC a well-tolerated chitosan-based adjuvant which induces the production of
CC anti-chorionic gonadotropin antibodies, without inducing the side effects
CC (e.g. hypersensitivity, erythema, etc.) associated with other adjuvants.
CC The vaccine also overcomes the problem of non-responsiveness in some
CC individuals. The present sequence represents a betahCG/beta-gal fusion
CC fused to an alpha-mating factor leader sequence at the N-terminus.
SQ Sequence 252 AA:

Query Match 100.0%; Score 1347; DB 21; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.1e-104;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRPSIFPAVLEFAASSALAAPVNTTDETAQIPAEAVIGSDLEGDFVAVLPFSNSTN 60
DB 1 MRPSITPAVLEFAASSALAAPVNTTDETAQIPAEAVIGSDLEGDFVAVLPFSNSTN 60
OY 61 NGLLFMTTASIAAKEEGVLEKREAEAVVERDPCGRDLKEPLRRCRPIATLAVEKE 120
DB 61 NGLLFMTTASIAAKEEGVLEKREAEAVVERDPCGRDLKEPLRRCRPIATLAVEKE 120
OY 121 GCPVCIVNTTACGCPMTRVLOGVLPALPQVVCNRYDVFESIRLPGRGVNPVYS 180
DB 121 GCVVCTIVNTTACGCPMTRVLOGVLPALPQVVCNRYDVFESIRLPGRGVNPVYS 180
OY 181 YAAVALSCOCALCRSTTDCGPKRHLPTCDPFRDSSSKAPPSRLPGSPDTP 240
DB 181 YAAVALSCOCALCRSTTDCGPKRHLPTCDPFRDSSSKAPPSRLPGSPDTP 240
OY 241 ILPOTSHNNHHN 252
DB 241 ILPOTSHNNHHN 252

RESULT 2

AAV57315 standard; Protein: 176 AA.

AAV57315;

19-JUN-2000 (first entry)

Human betahCG/beta-gal fusion protein.

Human chorionic gonadotropin: hCG; betahCG; vaccine: chitosan;

infertility; betahCG/beta-gal; fusion protein.

Homo sapiens.

WO200015253-A1.

23-MAR-2000.

16-SEP-1999; 99WO-US21591.

17-SEP-1998; 98US-0100766.

(ZONA-) ZONAGEN INC.

Harris J, Martinez M;

WPI: 2000-271258/23.

N-PSDB: AAV57315.

Novel human beta-subunit chorionic gonadotropin vaccines used to

PT Interrupt fertility in mammals by the immunological inactivation of the
PT pregnancy hormone chorionic gonadotropin
XX Claim 5: Page 32-33; 39pp; English.

CC The invention provides novel vaccine compositions which comprise the
CC beta-subunit of human chorionic gonadotropin (betahCG) in combination
CC with chitosan-based adjuvants. The vaccines are used to induce
CC infertility especially transient infertility, in female mammals. The
CC compositions are also used for antibody production. The vaccines comprise
CC a well-tolerated chitosan-based adjuvant which induces the production of
CC anti-chorionic gonadotropin antibodies, without inducing the side effects
CC (e.g. hypersensitivity, erythema, etc.) associated with other adjuvants.
CC The vaccine also overcomes the problem of non-responsiveness in some
CC individuals. The present sequence represents a betahCG/beta-gal fusion
CC protein consisting of leaderless betahCG linked to a beta-gal fragment.
SQ Sequence 176 AA:

Query Match 65.8%; Score 886.5; DB 21; Length 176;
Best Local Similarity 93.6%; Pred. No. 2.2e-66;
Matches 161; Conservative 4; Mismatches 2; Indels 5; Gaps 1;

OY 80 VLEKREAEAVVERDPCGRDLKEPLRRCRPIATLAVEKEGCVITVNTTICAGCPT 139
DB 10 VVLDGRDWE-----NPGCRDLKEPLRRCRPIATLAVEKEGCVITVNTTICAGCPT 64
OY 140 MTRVLOGVLPALPQVVCNRYDVFESIRLPGRGVNPVYSAAVALSCOCALCRSTTDC 199
DB 65 MTRVLOGVLPALPQVVCNRYDVFESIRLPGRGVNPVYSAAVALSCOCALCRSTTDC 124
OY 200 GGPCKDHPITCDPFRDSSSKAPPSRLPGSPDTPILPOTSHNNHHN 251
DB 125 GGPCKDHPITCDPFRDSSSKAPPSRLPGSPDTPILPOTSHNNHHN 176

RESULT 3

AAV43292 standard; Protein: 273 AA.

AAV43292;

19-JAN-2000 (first entry)

HCG beta subunit-Jun fusion protein sequence.

Cysteine knot protein: protein formation; heterodimeric protein analog;

deglycosylated glycoprotein hormone; infertility; immunogen; antigen;

polycystic ovarian disease; hCG; human; chorionic gonadotropin;

beta subunit; therapy; Jun.

Homo sapiens.

Synthetic.

WO9953065-A1.

21-OCT-1999.

13-APR-1999; 99WO-US08018.

14-APR-1998; 98US-0059625.

(UYNE-) UNIV NEW JERSEY.

Moyle WR;

WPI: 1999-620431/53.

Methods for producing heterodimers, particularly analogues of hormones,
from subunits of cysteine knot proteins -
Example 6: Fig 19; 73pp; English.

CC This sequence is a fusion protein of HCG and Jun. The invention
 CC relates to a method of forming a cysteine knot protein (I) having alpha
 CC and beta-subunits comprising attaching a dimerisation domain (DD) to
 CC either the N-termini of both subunits or the N-terminus of the
 CC alpha-subunit and to the C-terminus of the beta-subunit and dimerising
 CC the products to form a heterodimeric protein analog (II). The method is
 CC used to produce analogues (agonists or antagonists) of deglycosylated
 CC glycoprotein hormones, potentially useful, e.g. for treating infertility
 CC where caused by polycystic ovarian disease (associated with excessive
 CC levels of luteinising hormone). Products that retain DD's are also useful
 CC as immunogens or antigens (since a DD may contain highly antigenic
 CC amino acid sequences). Attachment of a DD (which may be removed later)
 CC facilitates the formation of heterodimers, that have similar structures
 CC (and thus receptor-binding and immunogenic properties) to native dimers,
 CC and allows the combination of subunits that would otherwise combine
 CC poorly, or not at all. The N-terminal part of a glycoprotein hormone may
 CC be modified without loss of activity, and attachment of the DD reduces
 CC formation of homodimers. Heterodimers have longer circulation times in
 CC vivo than individual subunits.

XX Sequence 273 AA:

Query Match Best Local Similarity 59.7%; Score 804; DB 20; Length 273;

Matches 158; Conservative 15; Mismatches 26; Indels 44; Gaps 4;

OY 3 FPSIFTAFLFAASSALAPVNTTDEDETAQIPAEAVIGYSDLEGDFDAVLPFSNSTNG 62

DB 74 FPAVLESDDLTLSSSVTP-----SSPRPSE----- 99

OY 63 LRFINTTIAIAKEEGVSLKREAEAYVEFDPG-CRDLKEPLRPKRPINATLAVEKEG 121

DB 100 -----TVCNVNHPASSSTVYDKK-----IVPRDCKSKRSKEPLRPRCRPINATLAVEKEG 150

OY 122 CPVCITVNTTICAGYCPMTNRVLQGLPALPOVYCNRDVRFESIRLPGCGRGVNPVVS 181

DB 151 CPVCITVNTTICAGYCPMTNRVLQGLPALPOVYCNRDVRFESIRLPGCGRGVNPVVS 210

OY 182 AVALSCCALCRSTYDCGPKDHPILTCDDPRFODSSSSKAPPSPSLRPGSDPTPI 241

DB 211 AVALSCCALCRSTYDCGPKDHPILTCDDPRFODSSSSKAPPSPSLRPGSDPTPI 270

OY 242 LPQ 244

DB 271 LPQ 273

RESULT 4

AA43285 ID AAY43285 standard; Protein: 273 AA.

AC AAY43285;

DT 19-JAN-2000 (first entry)

DE HCG beta subunit-Jun fusion protein sequence.

XX Cysteine knot protein; protein formation; heterodimeric protein analog;

KW deglycosylated glycoprotein hormone; infertility; immunogen; antigen;

KM polycystic ovarian disease; hCG; human; chorionic gonadotrophin;

KM beta subunit; therapy; Jun.

XX Homo sapiens.

OS Synthetic.

PN MO9953065-A1.

PD 21-OCT-1999.

PF 13-APR-1999; 99WO-US08018.

PR 14-APR-1998; 98US-0059625.

XX

PA (UYNE-) UNIV NEW JERSEY.

XX Moyle WR;

DR WPI; 1999-620431/53.

PT Methods for producing heterodimers, particularly analogues of hormones,

XX from subunits of cysteine knot proteins -

XX Example 6; Fig 18; 73pp; English.

CC This sequence is a fusion protein of hCG and Jun. The invention
 CC relates to a method of forming a cysteine knot protein (I) having alpha
 CC and beta-subunits comprising attaching a dimerisation domain (DD) to
 CC either the N-termini of both subunits or the N-terminus of the
 CC alpha-subunit and to the C-terminus of the beta-subunit and dimerising
 CC the products to form a heterodimeric protein analog (II). The method is
 CC used to produce analogues (agonists or antagonists) of deglycosylated
 CC glycoprotein hormones, potentially useful, e.g. for treating infertility
 CC where caused by polycystic ovarian disease (associated with excessive
 CC levels of luteinising hormone). Products that retain DD's are also useful
 CC as immunogens or antigens (since a DD may contain highly antigenic
 CC amino acid sequences). Attachment of a DD (which may be removed later)
 CC facilitates the formation of heterodimers, that have similar structures
 CC (and thus receptor-binding and immunogenic properties) to native dimers,
 CC and allows the combination of subunits that would otherwise combine
 CC poorly, or not at all. The N-terminal part of a glycoprotein hormone may
 CC be modified without loss of activity, and attachment of the DD reduces
 CC formation of homodimers. Heterodimers have longer circulation times in
 CC vivo than individual subunits.

XX Sequence 273 AA:

Query Match Best Local Similarity 59.5%; Score 802; DB 20; Length 273;

Matches 158; Conservative 15; Mismatches 26; Indels 44; Gaps 4;

OY 3 FPSIFTAFLFAASSALAPVNTTDEDETAQIPAEAVIGYSDLEGDFDAVLPFSNSTNG 62

DB 74 FPAVLESDDLTLSSSVTP-----SSPRPSE----- 99

OY 63 LRFINTTIAIAKEEGVSLKREAEAYVEFDPG-CRDLKEPLRPKRPINATLAVEKEG 121

DB 100 -----TVCNVNHPASSSTVYDKK-----IVPRDCKSKRSKEPLRPRCRPINATLAVEKEG 150

OY 122 CPVCITVNTTICAGYCPMTNRVLQGLPALPOVYCNRDVRFESIRLPGCGRGVNPVVS 181

DB 151 CPVCITVNTTICAGYCPMTNRVLQGLPALPOVYCNRDVRFESIRLPGCGRGVNPVVS 210

OY 182 AVALSCCALCRSTYDCGPKDHPILTCDDPRFODSSSSKAPPSPSLRPGSDPTPI 241

DB 211 AVALSCCALCRSTYDCGPKDHPILTCDDPRFODSSSSKAPPSPSLRPGSDPTPI 270

OY 242 LPQ 244

DB 271 LPQ 273

RESULT 5

AA43299 ID AAY43299 standard; Protein: 209 AA.

AC AAY43299;

DT 19-JAN-2000 (first entry)

DE HCG beta subunit-Jun fusion protein sequence.

XX Cysteine knot protein; protein formation; heterodimeric protein analog;

KW deglycosylated glycoprotein hormone; infertility; immunogen; antigen;

KM polycystic ovarian disease; hCG; human; chorionic gonadotrophin;

KM beta subunit; therapy; Jun.

XX

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OS Homo sapiens.
OS Synthetic.
XX WO9953065-A1.
XX
XX 21-OCT-1999.
XX
XX 13-APR-1999; 99WO-US08018.
XX
XX 14-APR-1998; 98US-0059625.
XX
XX (UYNE-) UNIV NEW JERSEY.
XX
XX Moyle WR.
XX
XX WPI; 1999-620431/53.
XX
XX Methods for producing heterodimers, particularly analogues of hormones,
XX from subunits of cysteine knot proteins.
XX
XX Example 7; Fig 20; 73pp; English.
XX
XX This sequence is a fusion protein of HCG and Jun. The invention
XX relates to a method of forming a cysteine knot protein (I) having alpha
XX and beta-subunits comprising attaching a dimerisation domain (DD) to
XX either the N-termini of both subunits or the N-terminus of the
XX alpha-subunit and to the C-terminus of the beta-subunit and dimerising
XX the products to form a heterodimeric protein analog (II). The method is
XX used to produce analogues (agonists or antagonists) of deglycosylated
XX glycoprotein hormones, potentially useful, e.g. for treating infertility
XX where caused by polycystic ovarian disease (associated with excessive
XX levels of luteinising hormone). Products that retain DD's are also useful
XX as immunogens or antigens (since a DD may containing highly antigenic
XX amino acid sequences). Attachment of a DD (which may be removed later)
XX facilitates the formation of heterodimers, that have similar structures
XX (and thus receptor-binding and immunogenic properties) to native dimers,
XX and allows the combination of subunits that would otherwise combine
XX poorly, or not at all. The N-terminal part of a glycoprotein hormone may
XX be modified without loss of activity, and attachment of the DD reduces
XX formation of homodimers. Heterodimers have longer circulation times in
XX vivo than individual subunits.
XX
XX Sequence 209 AA:
XX
XX Query Match 59.0%; Score 795; DB 20; Length 209;
XX Best Local Similarity 99.3%; Pred. No. 1.2e-58;
XX Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 101 KEPLRPRCPINATLAVKEGCPVCITVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 160
XX |
XX Db 22 KEPLRPRCPINATLAVKEGCPVCITVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 81
XX
XX QY 161 VRESIRLPGCGPRGVNPVSYAVALSCQALCRSTTDCGPGKHPDLTCDPRRQSSSS 220
XX |
XX Db 82 VRESIRLPGCGPRGVNPVSYAVALSCQALCRSTTDCGPGKHPDLTCDPRRQSSSS 141
XX
XX QY 221 KAPPSLPSPSRRLPGPSDTPILPOTS 246
XX |
XX Db 142 KAPPSLPSPSRRLPGPSDTPILPOTS 167
XX
XX RESULT 6
XX AA043304
XX ID AA043304 standard; Protein; 212 AA.
XX
XX AC AA043304;
XX
XX DT 19-JAN-2000 (first entry)
XX
XX DE HCG beta subunit-Jun fusion protein sequence.
XX
XX Cysteine knot protein; protein formation; heterodimeric protein analog;
XX deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
XX
XX

```

```

KW polycystic ovarian disease; hCG; human; chorionic gonadotropin;
KW beta subunit; therapy; Jun.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO9953065-A1.
XX
XX 21-OCT-1999.
XX
XX 13-APR-1999; 99WO-US08018.
XX
XX 14-APR-1998; 98US-0059625.
XX
XX (UYNE-) UNIV NEW JERSEY.
XX
XX Moyle WR.
XX
XX WPI; 1999-620431/53.
XX
XX Methods for producing heterodimers, particularly analogues of hormones,
XX from subunits of cysteine knot proteins.
XX
XX Example 7; Fig 20; 73pp; English.
XX
XX This sequence is a fusion protein of HCG and Jun. The invention
XX relates to a method of forming a cysteine knot protein (I) having alpha
XX and beta-subunits comprising attaching a dimerisation domain (DD) to
XX either the N-termini of both subunits or the N-terminus of the
XX alpha-subunit and to the C-terminus of the beta-subunit and dimerising
XX the products to form a heterodimeric protein analog (II). The method is
XX used to produce analogues (agonists or antagonists) of deglycosylated
XX glycoprotein hormones, potentially useful, e.g. for treating infertility
XX where caused by polycystic ovarian disease (associated with excessive
XX levels of luteinising hormone). Products that retain DD's are also useful
XX as immunogens or antigens (since a DD may containing highly antigenic
XX amino acid sequences). Attachment of a DD (which may be removed later)
XX facilitates the formation of heterodimers, that have similar structures
XX (and thus receptor-binding and immunogenic properties) to native dimers,
XX and allows the combination of subunits that would otherwise combine
XX poorly, or not at all. The N-terminal part of a glycoprotein hormone may
XX be modified without loss of activity, and attachment of the DD reduces
XX formation of homodimers. Heterodimers have longer circulation times in
XX vivo than individual subunits.
XX
XX Sequence 212 AA:
XX
XX Query Match 59.0%; Score 795; DB 20; Length 212;
XX Best Local Similarity 99.3%; Pred. No. 1.2e-58;
XX Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 101 KEPLRPRCPINATLAVKEGCPVCITVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 160
XX |
XX Db 22 KEPLRPRCPINATLAVKEGCPVCITVNTTICAGYCPMTFRVLOGVLPALPOVCNRYD 81
XX
XX QY 161 VRESIRLPGCGPRGVNPVSYAVALSCQALCRSTTDCGPGKHPDLTCDPRRQSSSS 220
XX |
XX Db 82 VRESIRLPGCGPRGVNPVSYAVALSCQALCRSTTDCGPGKHPDLTCDPRRQSSSS 141
XX
XX QY 221 KAPPSLPSPSRRLPGPSDTPILPOTS 246
XX |
XX Db 142 KAPPSLPSPSRRLPGPSDTPILPOTS 167
XX
XX RESULT 7
XX AA04602
XX ID AA04602 standard; Protein; 265 AA.
XX
XX AC AA04602;
XX
XX DT 23-OCT-2001 (first entry)
XX
XX DE Single chain gonadotropin analogue #1.
XX

```


Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 KEPLRPRCPRI~~NT~~LAVERKGCPCVITVNTTICAGYCPMT~~RV~~LG~~SV~~LPALPOVCN~~RD~~ 160
 DB 22 KEPLRPRCPRI~~NT~~LAVERKGCPCVITVNTTICAGYCPMT~~RV~~LG~~SV~~LPALPOVCN~~RD~~ 81
 QY 161 VRFESIRLPGCCPRGVPVSYAVALSOCALCRSTTDCGK~~PH~~PLTCDDPRFQDSSSS 220
 DB 82 VRFESIRLPGCCPRGVPVSYAVALSOCALCRSTTDCGK~~PH~~PLTCDDPRFQDSSSS 141
 QY 221 KAPPSLPSPSR~~LP~~GPSD~~PI~~LPQTS 246
 DB 142 KAPPSLPSPSR~~LP~~GPSD~~PI~~LPQTS 167

RESULT 9
 AAE04474
 ID AAE04474 standard; Protein: 265 AA.
 AC AAE04474;
 XX
 XX
 DT 04-SEP-2001 (first entry)
 DE Human single chain gonadotropin analog no:1.
 XX
 KW Human; single chain gonadotropin analog no:1; anti-infertility; drug;
 KW FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
 KW glycoprotein; infertility; fusion protein.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT Location/Qualifiers
 FT 21..165
 FT /note= "Corresponds to 1-145 amino acids of human
 FT chorionic gonadotropin (CG) beta-subunit"
 FT Region
 FT 166..173
 FT /note= "Linker peptide"
 FT 174..265
 FT /note= "Corresponds to 1-92 amino acids of human single
 FT chain gonadotropin alpha-subunit"
 FT
 FT
 PN US6238890-B1.
 XX
 PD 29-MAY-2001.
 XX
 PF 25-AUG-1997; 97US-0918288.
 XX
 PR 18-FEB-1994; 94US-0199382.
 PR 12-AUG-1994; 94US-0289396.
 PR 22-SEP-1994; 94US-0310590.
 PR 04-NOV-1994; 94US-0334628.
 PR 07-DEC-1994; 94US-0351591.
 PR 07-JUN-1995; 95US-0475049.
 PR 09-MAY-1997; 97US-0853524.
 XX
 PA (UNITV) UNITV WASHINGTON.
 XX
 PI Bolime I, Moyle WR;
 XX
 DR WPI: 2001-366474/38.
 DR N-PSDB: AAD08785.
 XX
 XX
 PT New DNA or RNA encoding single chain protein useful in treating
 PT infertility, as aids in vitro fertilization techniques, or other
 PT therapeutic methods associated with the native hormones
 PS
 PS Claim 9; Fig 5; 87pp: English.
 CC
 CC The invention relates to human single chain forms of the glycoprotein
 CC hormone quartet which is an agonist or antagonist of luteinising hormone
 CC (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone

CC (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
 CC having identical alpha subunits and differing beta subunits. The agonist
 CC forms of single chain hormones are used in treating infertility, as aids
 CC in vitro fertilisation techniques, and other therapeutic methods
 CC associated with the native hormones. The single chain hormones are useful
 CC as reagents in a manner similar to heterodimers, as diagnostic tools to
 CC detect the presence of antibodies with respect to the native proteins in
 CC biological samples, as control reagents in assay kits for assessing the
 CC levels of these hormones in various samples, in detecting and purifying
 CC receptors to which the native hormones bind. The single chain hormones
 CC are also used in affinity chromatographic preparation of receptors or
 CC antihormone antibodies. They are used as purification tools for
 CC isolation of subsequent preparations of these materials and to monitor
 CC glycoproteins are used to generate antibodies specifically immunoreactive
 CC with these new compounds, as substitutes for the heterodimeric forms of
 CC hormones. The present sequence is human single chain gonadotropin analog
 CC no:1 related to the invention. Analog no:1 is a fusion protein consisting
 CC of human chorionic gonadotropin (CG) beta-subunit (1-145 amino acids)
 CC fused to human single chain gonadotropin alpha-subunit (1-92 amino acids)
 CC by a linker sequence. This analog serves as a useful starting compound
 CC for template directed vaccine design and for the development of hormone-
 CC specific vaccines for use in humans.
 SQ Sequence 265 AA;
 Query Match 59.0%; Score 795; DB 22; Length 265;
 Best Local Similarity 99.3%; Pred. No. 1.5e-58;
 Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 KEPLRPRCPRI~~NT~~LAVERKGCPCVITVNTTICAGYCPMT~~RV~~LG~~SV~~LPALPOVCN~~RD~~ 160
 DB 22 KEPLRPRCPRI~~NT~~LAVERKGCPCVITVNTTICAGYCPMT~~RV~~LG~~SV~~LPALPOVCN~~RD~~ 81
 QY 161 VRFESIRLPGCCPRGVPVSYAVALSOCALCRSTTDCGK~~PH~~PLTCDDPRFQDSSSS 220
 DB 82 VRFESIRLPGCCPRGVPVSYAVALSOCALCRSTTDCGK~~PH~~PLTCDDPRFQDSSSS 141
 QY 221 KAPPSLPSPSR~~LP~~GPSD~~PI~~LPQTS 246
 DB 142 KAPPSLPSPSR~~LP~~GPSD~~PI~~LPQTS 167

RESULT 10
 AAE04486
 ID AAE04486 standard; Protein: 265 AA.
 AC AAE04486;
 XX
 XX
 DT 04-SEP-2001 (first entry)
 DE Human single chain gonadotropin analog no:1a.
 XX
 KW Human; single chain gonadotropin analog no:1a; anti-infertility; drug;
 KW peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
 KW FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
 KW glycoprotein; infertility; fusion protein; mutant; mutein.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT Location/Qualifiers
 FT 21..165
 FT /note= "Corresponds to 1-145 amino acids of human
 FT chorionic gonadotropin (CG) beta-subunit"
 FT Region
 FT 166..173
 FT /note= "Linker peptide"
 FT 174..265
 FT /note= "Corresponds to 1-92 amino acids of human single
 FT chain gonadotropin alpha-subunit"
 FT
 FT
 FT Misc-difference 225
 FT /note= "Wild type Asn substituted with Gln"

AC AAW95520:
 XX
 XX 24-MAR-1999 (first entry)
 XX Human chorionic gonadotropin (hCG) beta subunit.
 DE
 XX
 XX Human; chorionic gonadotropin; hCG; three-dimensional; 3D; analogue;
 KW molecular simulation; visual display; chemical structure; growth factor;
 KW N-glycosylation site; follicle stimulating hormone; luteinising hormone;
 KW thyroid stimulating hormone; in vitro fertilisation; fertility; mutation;
 KW beta subunit; glycoprotein.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 64 /note= "wild-type Phe at this position can be mutated
 FT to Asn to introduce a new N-glycosylation site;
 FT see claim 3"
 FT Misc-difference 79 /note= "wild-type Val at this position can be mutated
 FT to Asn to introduce a new N-glycosylation site;
 FT see claim 3"
 XX
 XX US5864488-A.
 XX 26-JAN-1999.
 XX 24-FEB-1995; 95US-0395238.
 XX 24-FEB-1994; 94GB-0003600.
 XX (UNIU) UNIV GLASGOW.
 PA
 PI Grooteenhuis PDJ, Harris DC, Isaacs NW, Laphorn AJ;
 XX WPI: 1999-131522/11.
 DR
 XX Determining the 3-dimensional coordinates of chorionic gonadotropin
 PT and computer-assisted re-design of the chemical structure - used for
 PT production of gonadotropin hormone analogues
 XX
 XX Examples; Fig 2; 60pp; English.
 PS
 XX The invention relates to determining whether an analogue of human
 CC chorionic gonadotropin (hCG) will have an altered three-dimensional (3D)
 CC structure as compared to hCG. Analogues of hCG and other glycoprotein
 CC hormones are produced by inputting chemical changes to the 3D structure
 CC into a computer loaded with 3D molecular simulation software and
 CC representing visually on a computer display. On inputting into the data
 CC input of the computer at least one operator change in chemical structure
 CC of the hCG molecule, the molecular simulation software produces a
 CC modified 3D molecular representation of the analogue structure. The 3D
 CC representation of the analogue can be displayed on the visual display,
 CC whereby changes in 3D structure of the hCG molecule consequent on changes
 CC in chemical structure can be visually determined. Glycoprotein analogues
 CC with additional glycosylation sites, and analogues with non-essential
 CC hairpins deleted can be produced by this method. The methods can be used
 CC to obtain analogues of hCG, follicle stimulating hormone, luteinising
 CC hormone, thyroid stimulating hormone, which may act as agonists or
 CC antagonists. The analogues can be used as growth factors in mammals, for
 CC in vitro fertilisation techniques and for treatment in vivo to enhance
 CC fertility. The present sequence represents the beta subunit of hCG.
 CC N-glycosylation sites can be introduced by single point mutations at
 CC specified positions to produce hCG analogues.
 XX
 SO Sequence 145 AA:
 Query Match 58.9%; Score 793; DB 20; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.1e-58;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 KEPLRRCRPIINATLAVEKEGCPVCIIVNTTICAGYCPMTIRVLQGVLPALPQVVCNRYD 160

DB 2 KEPLRRCRPIINATLAVEKEGCPVCIIVNTTICAGYCPMTIRVLQGVLPALPQVVCNRYD 61
 QY 161 VFEESIRLPGCRGVNPNVSAVALSCCALCRSTCCGGRKHPLTCDDPRFQDSSSS 220
 DB 62 VFEESIRLPGCRGVNPNVSAVALSCCALCRSTTCGGRKHPLTCDDPRFQDSSSS 121
 QY 221 KAPPSLPSPSRLPSPDTPILPQ 244
 DB 122 KAPPSLPSPSRLPSPDTPILPQ 145
 RESULT 13
 AAB20558
 ID AAB20558 standard; protein; 145 AA.
 XX
 AC AAB20558:
 XX
 DT 11-DEC-2000 (first entry)
 XX
 XX Human chorionic gonadotropin beta subunit amino acid sequence.
 DE
 XX Human; chorionic gonadotropin antigen; follicle stimulating hormone;
 KW contraception; abortion; hormone related disease; carcinoma; cytostatic;
 KW contraceptive; antifertility; antihypertensive; antidiabetic; vaccine;
 KW fertility; cancer; hypertension; diabetes.
 KW
 XX Homo sapiens.
 OS
 XX US6096318-A.
 PN
 XX 01-AUG-2000.
 PD
 XX 06-JUN-1995; 95US-0466445.
 PF
 XX 25-AUG-1978; 78US-0936876.
 PR 15-JUL-1987; 87US-0073748.
 PR 26-AUG-1992; 92US-0935331.
 PR 17-FEB-1989; 89US-0311331.
 PR 07-MAY-1973; 73US-0357892.
 PR 16-OCT-1973; 73US-0406821.
 PR 22-APR-1974; 74US-0462955.
 PR 14-OCT-1975; 75US-0622031.
 PR 16-JAN-1980; 80US-0112628.
 PR 20-NOV-1981; 81US-0323690.
 PR 18-MAY-1983; 83WO-US00777.
 PR 02-NOV-1984; 84US-0667863.
 PA
 PI (OHIS) UNIV OHIO STATE.
 PI Stevens VC;
 XX WPI: 2000-542298/49.
 DR
 XX New antigen for treating hormone related diseases, is conjugated with a
 PT specific polypeptide which elicits an antibody response against human
 PT chorionic gonadotropin -
 XX
 PS Disclosure; Column 18; 61pp; English.
 XX
 XX The present invention describes an antigen (A) comprising a carrier
 CC chemically conjugated with a polypeptide (I) capable of eliciting
 CC antibody response to human chorionic gonadotropin (CG) and not to human
 CC luteinising hormone (LH), or a polypeptide (II) capable of eliciting
 CC antibody response to human CG. (A) has cytostatic, contraceptive,
 CC antifertility, antihypertensive and antidiabetic activities, and can
 CC be used as part of a vaccine. (A) is useful for contraception, abortion
 CC and for treating hormone related diseases, for treating hormone
 CC associated carcinomas and to boost an animals' resistance to exogenous
 CC proteins e.g. viral proteins. (A) is also useful in animal fertility
 CC control, for treating cancer, hypertension, diabetes and related vascular
 CC diseases. (A), safely and effectively controls various disease states
 CC or maladies caused or influenced by unusual excesses of certain

CC polypeptides such as gastrin, angiotensin II or somatomedin. It also
 CC provides an effective and safe method of terminating a pregnancy soon
 CC after conception which does not have serious harmful side effects.
 CC The present sequence represents the human CG beta subunit amino acid
 CC sequence, which is given in the exemplification of the present
 CC invention.

XX Sequence 145 AA;

Query Match 58.9%; Score 793; DB 21; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.1e-58;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 KEPLRRCRPIINATLAVEKEGCPVCTIVNTTICAGYCPMTIRVLQGLPALPQVCNRYD 160
 DB 2 KEPLRRCRPIINATLAVEKEGCPVCTIVNTTICAGYCPMTIRVLQGLPALPQVCNRYD 61
 OY 161 VFESIRLPGCGRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPRLTCDPFRDSSSS 220
 DB 62 VFESIRLPGCGRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPRLTCDPFRDSSSS 121
 OY 221 KAPPSLPSPSRRLPGSPDPILPQ 244
 DB 122 KAPPSLPSPSRRLPGSPDPILPQ 145

RESULT 14
 AAU04619
 ID AAU04619 standard; protein; 145 AA.

XX AC AAU04619;

XX DT 23-OCT-2001 (first entry)

XX DE Human chorionic gonadotropin (hCG) beta, amino acids 1-145.

XX KM Human; chorionic gonadotropin; hCG; glycoprotein hormone; infertility;

XX KW luteinizing hormone; LH; follicle stimulating hormone; FSH;

XX KM thyroid stimulating hormone; TH.

XX OS Homo sapiens.

XX PN US6242580-B1.

XX PD 05-JUN-2001.

XX PF 31-MAR-1999; 990S-0282357.

XX PR 25-AUG-1997; 970S-0918288.

XX PR 18-FEB-1994; 940S-0199382.

XX PR 12-AUG-1994; 940S-0289396.

XX PR 22-SEP-1994; 940S-0310590.

XX PR 04-NOV-1994; 940S-0334628.

XX PR 07-DEC-1994; 940S-0351591.

XX PR 07-JUN-1995; 950S-0475049.

XX PR 09-MAY-1997; 970S-0853524.

XX PA (UNIT) UNIV WASHINGTON.

XX PI Boime I, Moyle WR;

XX DR WPI; 2001-424301/45.

XX PT New single chain forms of the glycoprotein hormone quarter useful for
 XX PT generating antibodies specifically immunoreactive with the new
 XX PT compounds, in treating infertility, or as aids for in vivo
 XX PT fertilization techniques
 XX PS Example 19; Column 34; 86pp; English.
 XX CC The sequence represents the amino acid sequence of human chorionic
 XX CC gonadotropin (hCG) beta, amino acids 1-145. The protein is an
 XX CC important glycoprotein hormone heterodimer, along with luteinizing

CC hormone (LH), follicle stimulating hormone (FSH), thyroid stimulating
 CC hormone (TH), which all have identical alpha subunits but differing beta
 CC subunits. The proteins are useful for generating antibodies specifically
 CC immunoreactive with new compounds, as substitutes for the
 CC heterodimeric forms of the hormones, in the treatment of infertility, as
 CC aids for in vivo fertilisation techniques, and in other therapeutic
 CC methods associated with the native hormones. The single chain proteins
 CC are further useful as reagents in a manner similar to the heterodimers,
 CC as diagnostic tools to detect the presence of antibodies with respect to
 CC the native proteins in the biological samples, as control reagents in
 CC assay kits for assessing the levels of these hormones in various samples,
 CC and in detecting and purifying receptors to which the native hormones
 CC bind. The single chain forms of the heterodimers or homodimers have the
 CC following advantages over their dimeric forms: they are more stable,
 CC problems of recombinant production are reduced since only a single gene
 CC is needed to transcribe, translate and process, provide an alternate form
 CC thus permitting fine tuning of activity levels and of in vivo half lives.
 CC Single chain forms are unique starting materials for identifying
 CC truncated forms with the activity of the dimer. The linkage between the
 CC subunits permits the protein to be engineered without disturbing the
 CC overall folding of the protein.

SO Sequence 145 AA;
 Query Match 58.9%; Score 793; DB 22; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.1e-58;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 KEPLRRCRPIINATLAVEKEGCPVCTIVNTTICAGYCPMTIRVLQGLPALPQVCNRYD 160
 DB 2 KEPLRRCRPIINATLAVEKEGCPVCTIVNTTICAGYCPMTIRVLQGLPALPQVCNRYD 61
 OY 161 VFESIRLPGCGRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPRLTCDPFRDSSSS 220
 DB 62 VFESIRLPGCGRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPRLTCDPFRDSSSS 121

OY 221 KAPPSLPSPSRRLPGSPDPILPQ 244
 DB 122 KAPPSLPSPSRRLPGSPDPILPQ 145

RESULT 15
 AAEO4491
 ID AAEO4491 standard; protein; 145 AA.

XX AC AAEO4491;

XX DT 04-SEP-2001 (first entry)

XX DE Human chorionic gonadotropin beta-subunit fragment (1-145 amino acids).

XX KM Human; single chain gonadotropin analog; anti-infertility; drug;

XX KW peptide therapy; luteinizing hormone; LH; follicle stimulating hormone;

XX KW FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;

XX KW glycoprotein; infertility; fusion protein.

XX OS Homo sapiens.

XX PN US6238890-B1.

XX PD 29-MAY-2001.

XX PF 25-AUG-1997; 970S-0918288.

XX PR 18-FEB-1994; 940S-0199382.

XX PR 12-AUG-1994; 940S-0289396.

XX PR 22-SEP-1994; 940S-0310590.

XX PR 04-NOV-1994; 940S-0334628.

Location/Qualifiers
 key
 MISC-difference 145
 /note- "Residue 'O' is present at this location in the
 sequence shown in column 33 of the specification"

PR 07-DEC-1994; 94US-0351591.
 PR 07-JUN-1995; 95US-0475049.
 PR 09-MAY-1997; 97US-0853524.

XX
 PA (UNIM) UNIV WASHINGTON.

XX
 PI Bolme I, Moyle WR:

XX
 DR WPI; 2001-366474/38.

XX
 PT New DNA or RNA encoding single chain protein useful in treating
 PT infertility, as aids in vitro fertilization techniques, or other
 PT therapeutic methods associated with the native hormones

PS Example 19; Column 103-106; 87pp; English.

XX
 CC The invention relates to human single chain forms of the glycoprotein
 CC hormone quarter which is an agonist or antagonist of luteinizing hormone
 CC (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
 CC (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
 CC having identical alpha subunits and differing beta subunits. The agonist
 CC forms of single chain hormones are used in treating infertility, as aids
 CC in vitro fertilisation techniques, and other therapeutic methods
 CC associated with the native hormones. The single chain hormones are useful
 CC as reagents in a manner similar to heterodimers, as diagnostic tools to
 CC detect the presence of antibodies with respect to the native proteins in
 CC biological samples, as control reagents in assay kits for assessing the
 CC levels of these hormones in various samples, in detecting and purifying
 CC receptors to which the native hormones bind. The single chain hormones
 CC are also used in affinity chromatographic preparation of receptors or
 CC antihormone antibodies. They are used as purification tools for
 CC isolation of subsequent preparations of these materials and to monitor
 CC levels of single chain hormones administered as drugs. The single chain
 CC glycoproteins are used to generate antibodies specifically immunoreactive
 CC with these new compounds, as substitutes for the heterodimeric forms of
 CC hormones. The present sequence is human chorionic gonadotropin beta-
 CC subunit fragment (1-145 amino acids) which is used for constructing
 CC single chain gonadotropin analogs related to the invention. Analog
 CC fusion proteins serves as useful starting compounds for template directed
 CC vaccine design and for the development of hormone-specific vaccines for
 CC use in humans.

XX
 SQ Sequence 145 AA:

Query Match 58.9%; Score 793; DB 22; Length 145;
 Best Local Similarity 100.0%; Pred. No. 1.1e-58;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 101 KEPLRRCRPIINATLAVKEGCPVCITVNTTICAGYCPMTWRLQGLPALPOVVCNYRD 160
 |||||||
 DB 2 KEPLRRCRPIINATLAVKEGCPVCITVNTTICAGYCPMTWRLQGLPALPOVVCNYRD 61
 OY 161 VRFESIRLPGCGPRGVNPRVSYAVALSQCQALCRSTTDCGPKDHPDLTCDPRFODSSSS 220
 |||||||
 DB 62 VRFESIRLPGCGPRGVNPRVSYAVALSQCQALCRSTTDCGPKDHPDLTCDPRFODSSSS 121
 OY 221 KAPPPLSPSPRLPGSPDTPILPQ 244
 |||||||
 DB 122 KAPPPLSPSPRLPGSPDTPILPQ 145

Search completed: November 20, 2002, 17:27:36
 Job time : 38.1818 secs

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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:29:06 ; Search time 8.22378 Seconds

(without alignments)
479.913 Million cell updates/sec

Title: US-09-787-494-4

Perfect score: 1347
Sequence: 1 MRPESTITAVLFPAASALAA.....LPGSPDPILPOTSHHHHH 252Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 1566196 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCU_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	58.9	165	9	US-09-915-676-1 Sequence 1, Appli
2	793	58.9	165	10	US-09-466-320-14 Sequence 14, Appli
3	767	56.9	307	10	US-09-756-186-4 Sequence 4, Appli
4	767	56.9	336	10	US-09-756-186-8 Sequence 8, Appli
5	766	56.9	141	9	US-09-813-398-3 Sequence 3, Appli
6	611	45.4	195	10	US-09-780-933-30 Sequence 30, Appli
7	611	45.4	196	10	US-09-780-933-29 Sequence 29, Appli
8	540	40.1	122	9	US-09-813-398-4 Sequence 4, Appli
9	435	32.3	141	10	US-09-730-617-47 Sequence 47, Appli
10	432	32.1	462	10	US-09-846-729A-3 Sequence 3, Appli
11	432	32.1	464	10	US-09-846-729A-17 Sequence 17, Appli
12	432	32.1	464	10	US-09-846-729A-14 Sequence 14, Appli
13	425	31.6	141	10	US-09-829-549A-48 Sequence 48, Appli
14	416	30.9	611	10	US-09-740-359-7 Sequence 7, Appli
15	414.5	30.8	144	10	US-09-894-711-7 Sequence 7, Appli
16	414	30.7	144	10	US-09-894-711-7 Sequence 7, Appli
17	413.5	30.7	144	10	US-09-736-611-6 Sequence 6, Appli
18	413.5	30.7	144	10	US-09-740-359-5 Sequence 5, Appli
19	413.5	30.7	146	10	US-09-894-711-5 Sequence 5, Appli

20	413.5	30.7	147	10	US-09-736-611-8 Sequence 8, Appli
21	403.5	30.0	86	12	US-10-153-064-69 Sequence 69, Appli
22	403	29.9	155	10	US-09-921-398-39 Sequence 39, Appli
23	403	29.9	191	10	US-09-921-398-41 Sequence 41, Appli
24	380	28.2	113	10	US-09-730-617-44 Sequence 44, Appli
25	371	27.5	99	10	US-09-730-617-41 Sequence 41, Appli
26	303	22.5	140	10	US-09-730-617-46 Sequence 46, Appli
27	303	22.5	144	10	US-09-730-617-45 Sequence 45, Appli
28	265.5	19.7	116	10	US-09-730-617-38 Sequence 38, Appli
29	265	19.7	85	10	US-09-730-617-35 Sequence 35, Appli
30	247	18.3	119	9	US-09-813-398-2 Sequence 2, Appli
31	227	16.9	111	9	US-09-973-918A-4 Sequence 4, Appli
32	226	16.8	110	9	US-09-813-398-5 Sequence 5, Appli
33	215	16.0	108	9	US-09-973-918A-11 Sequence 11, Appli
34	215	16.0	109	9	US-09-973-918A-12 Sequence 12, Appli
35	215	16.0	110	9	US-09-973-918A-13 Sequence 13, Appli
36	215	16.0	111	9	US-09-973-918A-6 Sequence 6, Appli
37	215	16.0	111	9	US-09-973-918A-10 Sequence 10, Appli
38	215	16.0	111	10	US-09-780-933-4 Sequence 4, Appli
39	215	16.0	129	10	US-09-780-933-3 Sequence 3, Appli
40	215	16.0	129	10	US-09-780-933-23 Sequence 23, Appli
41	215	16.0	196	10	US-09-780-933-28 Sequence 28, Appli
42	209	15.5	111	9	US-09-973-918A-2 Sequence 2, Appli
43	208	15.4	111	9	US-09-973-918A-8 Sequence 8, Appli
44	204	15.1	38	9	US-09-913-676-3 Sequence 3, Appli
45	204	15.1	38	10	US-09-466-320-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-915-676-1
; Sequence 1, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-676-1

Query Match 58.9%; Score 793; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.1e-59;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRPRCRINATLAVEKGCVCITVNTTICAGTCPTWTRVLOGVLPALPOVVCNYRD 160
DB 22 KEPLRPRCRINATLAVEKGCVCITVNTTICAGTCPTWTRVLOGVLPALPOVVCNYRD 81
QY 161 VRESTRRLPCPCPGVNPVSYAVALSQCCLGRSTTDCGPKDHPITCDPFFODSSSS 220
DB 82 VRESTRRLPCPCPGVNPVSYAVALSQCCLGRSTTDCGPKDHPITCDPFFODSSSS 141
QY 221 KAPPSLPSPSRILPGSPDPIILPQ 244
DB 142 KAPPSLPSPSRILPGSPDPIILPQ 165

RESULT 2

US-09-466-320-14
Sequence 14, Application US/09466320
Patent No. US2002025939A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick
TITLE OF INVENTION: Chorioid Gonadotropin DNA Vaccines and
FILE REFERENCE: Methods
CURRENT APPLICATION NUMBER: US/09/466,320
CURRENT FILING DATE: 1999-12-17
EARLIER APPLICATION NUMBER: US 60/112,910
EARLIER FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 165
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hCG beta sub unit
US-09-466-320-14

Query Match
Best Local Similarity 58.9%; Score 793; DB 10; Length 165;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 KEPLRPRCPINATLAVEKEGCPVCTVNTTICAGYCPMTNRVLQGVLPALPOVVCNRYD 160
Db 22 KEPLRPRCPINATLAVEKEGCPVCTVNTTICAGYCPMTNRVLQGVLPALPOVVCNRYD 160
Qy 161 VRFESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPILCDPDRFODSSSS 220
Db 82 VRFESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPILCDPDRFODSSSS 220
Qy 221 KAPPSPSPSRLLPGSPDPIPLPQ 244
Db 142 KAPPSPSPSRLLPGSPDPIPLPQ 165

RESULT 3

US-09-756-186-4
Sequence 4, Application US/09756186
Patent No. US2001001433A1
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: CAMPBELL-2A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-756-186-4

Query Match
Best Local Similarity 56.9%; Score 767; DB 10; Length 307;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 PRCRPNATLAVEKEGCPVCTVNTTICAGYCPMTNRVLQGVLPALPOVVCNRYDREFS 165
Db 169 PRCRPNATLAVEKEGCPVCTVNTTICAGYCPMTNRVLQGVLPALPOVVCNRYDREFS 228
Qy 166 IRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPILCDPDRFODSSSSKAPP 225
Db 229 IRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPILCDPDRFODSSSSKAPP 288
Qy 226 SLSPSPSRLLPGSPDPIPLPQ 244
Db 289 SLSPSPSRLLPGSPDPIPLPQ 307

RESULT 4

US-09-756-186-8
Sequence 8, Application US/09756186
Patent No. US2001001433A1
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-756-186-8

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Query Match          56.9%; Score 767; DB 10; Length 336;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 PRCRPNATLAVEKEGCPVCTVNTTTCAGYCPMTRVLOGLPALPOVVCNRYD 165
      |||||||
DB 198 PRCRPNATLAVEKEGCPVCTVNTTTCAGYCPMTRVLOGLPALPOVVCNRYD 257
      |||||||

QY 166 IRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPDLTCDPRFODSSSKAPP 225
      |||||||
DB 258 IRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPDLTCDPRFODSSSKAPP 317
      |||||||

QY 226 SLSPSPRLPGPSDTPILPQ 244
      |||||||
DB 318 SLSPSPRLPGPSDTPILPQ 336
      |||||||

RESULT 5
US-09-813-398-3
; Sequence 3, Application US/09813398
; Patent No. US2002016292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: USFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 141
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-3

Query Match          56.9%; Score 766; DB 9; Length 141;
Best Local Similarity 100.0%; Pred. No. 3e-57;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRRCRPNATLAVEKEGCPVCTVNTTTCAGYCPMTRVLOGLPALPOVVCNRYD 160
      |||||||
DB 3 KEPLRRCRPNATLAVEKEGCPVCTVNTTTCAGYCPMTRVLOGLPALPOVVCNRYD 62
      |||||||

QY 161 VFESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPDLTCDPRFODSSSS 220
      |||||||
DB 63 VFESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPDLTCDPRFODSSSS 122
      |||||||

QY 221 KAPPSLPSRLPGPSDT 239
      |||||||
DB 123 KAPPSLPSRLPGPSDT 141
      |||||||

RESULT 6
US-09-780-933-30
; Sequence 30, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMBYE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
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; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-933-30

Query Match          45.4%; Score 611; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.8e-44;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRRCRPNATLAVEKEGCPVCTVNTTTCAGYCPMTRVLOGLPALPOVVCNRYD 160
      |||||||
DB 86 KEPLRRCRPNATLAVEKEGCPVCTVNTTTCAGYCPMTRVLOGLPALPOVVCNRYD 145
      |||||||

QY 161 VFESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPDLTCD 210
      |||||||
DB 146 VFESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPDLTCD 195
      |||||||

RESULT 7
US-09-780-933-29
; Sequence 29, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMBYE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-933-29

Query Match          45.4%; Score 611; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 3.9e-44;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRRCRPNATLAVEKEGCPVCTVNTTTCAGYCPMTRVLOGLPALPOVVCNRYD 160
      |||||||
DB 87 KEPLRRCRPNATLAVEKEGCPVCTVNTTTCAGYCPMTRVLOGLPALPOVVCNRYD 146
      |||||||

QY 161 VFESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPDLTCD 210
      |||||||
DB 147 VFESIRLPGCPRGVNPVSYAVALSQCACLCRRSTTDCGPKDHPDLTCD 196
      |||||||

RESULT 8
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US-09-813-398-4
 ; Sequence 4, Application US/09813398
 ; Patent No. US20020169292A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruce D. Weintraub
 ; APPLICANT: Mariusz W. Szkludlinski
 ; APPLICANT: University of Maryland
 ; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
 ; FILE REFERENCE: USFMD.003C1
 ; CURRENT APPLICATION NUMBER: US/09/813,398
 ; CURRENT FILING DATE: 2001-03-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/05908
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: PCT/US98/19772
 ; PRIOR FILING DATE: 1998-09-22
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 122
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIEN
 US-09-813-398-4

Query Match
 Best Local Similarity 40.1%; Score 540; DB 9; Length 122;
 Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

OY 101 KEPLRPRCPINATLAVEKEGCPVCITVNTTTCAGTCPTMTRYLOGVLPALPQVNCNRD 160
 DB 3 REPLRPMCHPINALLAVEKEGCPVCITVNTTTCAGTCPTMTRYLOGVLPALPQVNCNRD 160
 OY 161 VRFESILRCPGRGVNPNVSYAVALSCQCALCRSTTDCGGPKDHPDLCDDPR 213
 DB 63 VRFESILRCPGRGVNPNVSYAVALSCQCALCRSTTDCGGPKDHPDLCDDPR 213
 US-09-730-617-47

RESULT 9
 ; US-09-730-617-47
 ; Sequence 47, Application US/09730617
 ; Patent No. US20020068279A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Prayaga, Sudhirdas K
 ; APPLICANT: Shinkels, Richard A
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Zerhusen, Bryan D
 ; APPLICANT: Mezes, Peter S
 ; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
 ; FILE REFERENCE: 15966-609
 ; CURRENT APPLICATION NUMBER: US/09/730,617
 ; CURRENT FILING DATE: 2000-12-05
 ; PRIOR APPLICATION NUMBER: 60/169,056
 ; PRIOR FILING DATE: 1999-12-06
 ; PRIOR APPLICATION NUMBER: 60/169,886
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: 60/169,866
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: 60/170,252
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: 60/175,740
 ; PRIOR FILING DATE: 2000-01-12
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 141
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 US-09-730-617-47

Query Match
 Best Local Similarity 32.3%; Score 435; DB 10; Length 141;
 Matches 75; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

OY 103 PLRPRCPINATLAVEKEGCPVCITVNTTTCAGTCPTMTRYLOGVLPALPQVNCNRD 162
 DB 24 PLRPRCPINATLAVEKEGCPVCITVNTTTCAGTCPTMTRYLOGVLPALPQVNCNRD 162
 OY 163 FESIRLPCGRGVNPNVSYAVALSCQCALCRSTTDCGGPKDHPDLCDDPR 216
 DB 84 FASIRLPCGRGVNPNVSYAVALSCQCALCRSTTDCGGPKDHPDLCDDPR 216
 US-09-846-729A-3

RESULT 10
 ; US-09-846-729A-3
 ; Sequence 3, Application US/09846729A
 ; Patent No. US20020058322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Boone, Thomas
 ; APPLICANT: Li, HuiMin
 ; APPLICANT: Mann, Michael
 ; TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
 ; FILE REFERENCE: A-596
 ; CURRENT APPLICATION NUMBER: US/09/846,729A
 ; CURRENT FILING DATE: 2001-05-01
 ; PRIOR APPLICATION NUMBER: 09/411,329
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 462
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Native pro-NAT (analog of fibrolase)
 US-09-846-729A-3

Query Match
 Best Local Similarity 32.1%; Score 432; DB 10; Length 462;
 Matches 89; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 MRFPSITFAVFAASSALAPVNTTDETAQIPAEAVIGSLEDGEVAVLPFSNSTN 60
 DB 1 MRFPSITFAVFAASSALAPVNTTDETAQIPAEAVIGSLEDGEVAVLPFSNSTN 60
 OY 61 NGLEFINTTIAIAKEGVSLEKREAE 89
 DB 61 NGLEFINTTIAIAKEGVSLEKREAE 89
 US-09-846-729A-17

RESULT 11
 ; US-09-846-729A-17
 ; Sequence 17, Application US/09846729A
 ; Patent No. US20020058322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Boone, Thomas
 ; APPLICANT: Li, HuiMin
 ; APPLICANT: Mann, Michael
 ; TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
 ; FILE REFERENCE: A-596
 ; CURRENT APPLICATION NUMBER: US/09/846,729A
 ; CURRENT FILING DATE: 2001-05-01
 ; PRIOR APPLICATION NUMBER: 09/411,329
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 462
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Analog form of native pro-fibrolase of AgHistradon confortilix
 US-09-846-729A-17

Query Match
 Best Local Similarity 32.1%; Score 432; DB 10; Length 462;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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: NUMBER OF SEQ ID NOS: 100
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 48
: LENGTH: 141
: TYPE: PRT
: ORGANISM: Ovis aries
: US-09-730-617-48

Query Match
Best Local Similarity 64.9%; Pred. No. 8.3e-29;
Matches 74; Conservative 13; Mismatches 27; Indels 0; Gaps 0;

QY 103 PLRPRCPRIINMTLAVEKEGCPVCITVNTTICAGYCPTRVLYGVLPALPOVCNYPDVR 162
      |||:::||||| |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 24 PLRPLQCPQINMTLAEKACACPVCTFTTISICAGYCLSKRVLPVILPMPQRVCTYHELR 83

QY 163 FESIRLPCCPGVNPVSVYAVALSQCQALCRRTTDCGPGPDHPLTCDDPRFOD 216
      |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 84 FASVRLPCCPGVDPMVSFPAVLSCHGCRSLSTDCGGPRTPQPLACDHPPLPD 137

RESULT 14
US-09-829-549A-48
: Sequence 48, Application US/09829549A
: Patent NO. US20020052484A1
: GENERAL INFORMATION:
: APPLICANT: The Curators of the University of Missouri
: TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES
: FILE REFERENCE: UMO 1521.1
: CURRENT APPLICATION NUMBER: US/09/829,549A
: PRIOR FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: US 60/195,785
: PRIOR FILING DATE: 2000-04-10
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 48
: LENGTH: 611
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: SIGNAL
: LOCATION: (1)..(85)
: OTHER INFORMATION: Mat-alpha secretory sequence
: NAME/KEY: DOMAIN
: LOCATION: (86)..(600)
: OTHER INFORMATION: Cytokinin oxidase 1
: NAME/KEY: DOMAIN
: LOCATION: (601)..(602)
: OTHER INFORMATION: Linker
: NAME/KEY: DOMAIN
: LOCATION: (603)..(611)
: OTHER INFORMATION: Random peptide Pc 87
: US-09-829-549A-48

Query Match
Best Local Similarity 30.9%; Score 416; DB 10; Length 611;
Matches 93; Conservative 2; Mismatches 11; Indels 10; Gaps 2;

QY 1 MRPSIFATVAFSAASSALAAPVNTTDEDTQIPAAVIGYSDLEGDPDVAVLPSNSTN 60
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1 MRPSIFATVAFSAASSALAAPVNTTDEDTQIPADAVIGYSDLEGDPDVAVLPSNSTN 60

QY 61 NGLFINTTISIAAKEGVSLERREAAVVEFDGCGDLEPLRPKRPINATIA 116
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 61 NGLFINTTISIAAKEGVSLERREAAVVEFDGCGDLEPLRPKRPINATIA 106

RESULT 15
US-09-740-359-7
: Sequence 7, Application US/09740359
: Patent NO. US20010041787A1
: GENERAL INFORMATION:
: APPLICANT: Kjeldsen, Thomas Borjrum

```

```
; APPLICANT: Ludvigsen, Svend
; TITLE OF INVENTION: Method for making insulin precursors and
; TITLE OF INVENTION: Insulin precursor analogues having improved fermentation
; TITLE OF INVENTION: yield in yeast
; FILE REFERENCE: 6148,200-US
; CURRENT APPLICATION NUMBER: US/09/740,359
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PA 2000 00443
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: PA 1999 01869
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/211,081
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/181,450
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Alpha leader fused with N-terminally extended
US-09-740-359-7
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Query Match          30.8%; Score 414.5; DB 10; Length 147;
Best Local Similarity 67.3%; Pred. No. 6,6e-28;
Matches 99; Conservative 7; Mismatches 30; Indels 11; Gaps 4;

OY 1 MRFPSIFFAVLFAASSALAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPPSNSTN 60
   |||||
DB 1 MRFPSIFFAVLFAASSALAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPPSNSTN 60
   |||||

OY 61 NGLPINTTIIASIAKKEGVSLER---EAEA--YVEFDPCCRDILKEPLRPRCRPINATL 115
   |||||
DB 61 NGLPINTTIIASIAKKEGVSMARKEAEAPKFNQHLGSHLVLEALVWCE-RGEF 119
   |||||

OY 116 AVEKEGCPVCITVNTTICA----GYC 137
   |||
DB 120 YTDKDGKGIIVEQCTGICSLYQLENYC 146
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Search completed: November 20, 2002, 17:35:35
Job time : 9.22378 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 15.2727 Seconds
(without alignments)
485.478 Million cell updates/sec

Title: US-09-787-494-4
1347
Sequence: 1 MREPSIFTAVLFAASSALAA.....LPGSPDPRLLPQYSHNNHHN 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: /cgn2_6/ptodata/1/laa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/laa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	795	59.0	265	4	US-08-918-288-3
2	795	59.0	265	4	US-08-918-288-39
3	795	59.0	265	4	US-09-282-357-3
4	795	59.0	265	4	US-09-282-357-39
5	793	58.9	145	1	US-08-475-213-10
6	793	58.9	145	2	US-08-395-238-2
7	793	58.9	145	4	US-09-142-320-12
8	793	58.9	145	4	US-09-142-320-13
9	793	58.9	145	4	US-09-142-320-14
10	793	58.9	145	4	US-09-142-320-15
11	793	58.9	145	4	US-08-918-288-68
12	793	58.9	145	4	US-09-282-357-68
13	793	58.9	145	4	US-08-908-371B-1
14	790	58.6	165	2	US-08-709-924-2
15	790	58.6	165	2	US-08-709-925-2
16	790	58.6	165	4	US-08-709-948-2
17	789	58.6	181	4	US-08-918-288-36
18	789	58.6	181	4	US-09-282-357-36
19	787	58.4	145	1	US-08-425-673-1
20	787	58.4	145	1	US-08-425-673-2
21	787	58.4	145	1	US-08-298-189B-1
22	785	58.3	145	4	US-09-142-320-16
23	773	57.4	145	4	US-09-142-320-11
24	772	57.3	145	4	US-09-142-320-4
25	767	56.9	307	4	US-08-804-166-4
26	767	56.9	307	4	US-08-910-991-4
27	767	56.9	336	4	US-08-804-166-8

28	767	56.9	336	4	US-08-910-991-8	Sequence 8, Appl
29	766	56.9	145	1	US-08-425-673-10	Sequence 10, Appl
30	644	47.8	234	4	US-08-918-288-6	Sequence 6, Appl
31	644	47.8	234	4	US-09-282-357-6	Sequence 6, Appl
32	629	46.7	114	4	US-08-918-288-69	Sequence 69, Appl
33	629	46.7	114	4	US-09-282-357-69	Sequence 69, Appl
34	578	42.9	234	4	US-08-918-288-24	Sequence 24, Appl
35	578	42.9	234	4	US-09-282-357-24	Sequence 24, Appl
36	565	41.9	114	1	US-08-425-673-9	Sequence 9, Appl
37	557	41.4	114	1	US-08-425-673-7	Sequence 7, Appl
38	555	41.2	234	4	US-08-918-288-9	Sequence 9, Appl
39	555	41.2	234	4	US-09-282-357-9	Sequence 9, Appl
40	549	40.8	234	4	US-08-918-288-21	Sequence 21, Appl
41	549	40.8	234	4	US-09-282-357-21	Sequence 21, Appl
42	545	40.5	237	4	US-08-918-288-18	Sequence 18, Appl
43	545	40.5	237	4	US-09-282-357-18	Sequence 18, Appl
44	540	40.1	114	4	US-08-918-288-71	Sequence 71, Appl
45	540	40.1	114	4	US-09-282-357-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-08-918-288-3
; Sequence 3, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/282,357
; FILING DATE:
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mursahige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-918-288-3

Query Match	59.0%	Score	795	DB	4	Length	265
Best Local Similarity	99.3%	Pred. No.	2.5e-67				
Matches	145	Conservative	0	Mismatches	1	Indels	0
QY	101	KEPLRPCHRPINATLAVKEGCPVCITVNTTTCAGYCPMTREVLQGVLPALPQVCNVRD	160				
Db	22	KEPLRPCHRPINATLAVKEGCPVCITVNTTTCAGYCPMTREVLQGVLPALPQVCNVRD	81				
QY	161	VAFESIRLPGCGRGVNPVYSVAALSCQALCRSTTDCGKGRDHPLTCTDDPRFODSSS	220				
Db	82	VAFESIRLPGCGRGVNPVYSVAALSCQALCRSTTDCGKGRDHPLTCTDDPRFODSSS	141				
QY	221	KAPPSLPSPSRLPGPSDPIILPQTS	246				
Db	142	KAPPSLPSPSRLPGPSDPIILPQTS	167				

```

US-08-918-288-39
: Sequence 39, Application US/08918288
: Patent No. 623890
:
: GENERAL INFORMATION:
: APPLICANT: BOIME, Irving
: APPLICANT: MOYLE, William R.
: TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
: TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
: NUMBER OF SEQUENCES: 83
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Avenue, NW, suite 5500
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: PASCSEQ for Windows Version 2.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/918, 288
: FILING DATE:
: CLASSIFICATION:
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/282,357
: FILING DATE:
: APPLICATION NUMBER: 08/853,524
: FILING DATE: 09-MAY-1997
: APPLICATION NUMBER: 08/199,382
: FILING DATE: 18-FEB-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 29500-20050.25
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-887-1500
: TELEFAX: 202-887-0763
: TELEX:
:
: INFORMATION FOR SEQ ID NO: 39:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 265 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: Internal
:
US-08-918-288-39
Query Match 59.0%: Score 795; DB 4; Length 265;
Best Local Similarity 99.3%; Pred. NO.2.5e-67;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0

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QY	101	KEPLRRPRPINALTAVEKECPICITVNTTICAGYCEPTMMRVLOGLPALPOVVCNRYD	160
Db	22	KEPLRRPRPINALTAVEKECPICITVNTTICAGYCEPTMMRVLOGLPALPOVVCNRYD	81
QY	161	VFEESIRLPGCPGVNPNVSYAVALSCOCALCRSTTIDCGGPKHPLTCDDPRFODSSSS	220
Db	82	VFEESIRLPGCPGVNPNVSYAVALSCOCALCRSTTIDCGGPKHPLTCDDPRFODSSSS	141
QY	221	KAPPSLPSPSRLLPGSPDTPILPOTS	246
Db	142	KAPPSLPSPSRLLPGSPDTPILPOTS	167

```

RESULT 3
US-09-282-357-3
Sequence 3, Application US/09282357
Patent No. 6242580
GENERAL INFORMATION:
APPLICANT: BOJME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,357
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/918,288
FILING DATE: 25 AUG-1997
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-282-357-3

Query Match          59.0%; Score 795; DB 4; Length 265;
Best Local Similarity 99.3%; Pred. No. 2,5e-67;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 101 KEPLRRPCRPINATLAVEKGGCPVCITVNTTICAGYCPTMTRVLOGVLPALPOVNCYRD 160
Db 22 KEPLRRRCRPINATLAVEKGGCPVCITVNTTICAGYCPTMTRVLOGVLPALPOVNCYRD 81
Y 161 VRFESIRLPGCPRGVNVYAVVALSCOCALCRSTTDCGPKDHPJTCDDPFRDSSSS 220

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Db 82 VRESIRLPGCPRGVNVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFODSSSS 141
OY 221 KAPPSLSPSRRLGSPDTPILPOTS 246
Db 142 KAPPSLSPSRRLGSPDTPILPOTS 167

RESULT 4
US-09-282-357-39
; Sequence 39, Application US/09282357
; Patent No. 6242380
; GENERAL INFORMATION:
; APPLICANT: BOJME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282,357
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/918,288
; FILING DATE: 25 AUG-1997
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mareshige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-282-357-39

Query Match 59.0%; Score 795; DB 4; Length 265;
Best Local Similarity 99.3%; Pred. No. 2.5e-67;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 101 KEPLRPRCPINATLAVERKESCPVCITVNTTICAGYCPMTTRVLQGVLPALPOVVCNYRD 160
Db 22 KEPLRRCRPIINATLAVERKESCPVCITVNTTICAGYCPMTTRVLQGVLPALPOVVCNYRD 81
OY 161 VRESIRLPGCPRGVNVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
Db 82 VRESIRLPGCPRGVNVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFODSSSS 141
OY 221 KAPPSLSPSRRLGSPDTPILPOTS 246
Db 142 KAPPSLSPSRRLGSPDTPILPOTS 167

Db 142 KAPPSLSPSRRLGSPDTPILPOTS 167

RESULT 5
US-08-475-213-10
; Sequence 10, Application US/08475213
; Patent No. 5783674
; GENERAL INFORMATION:
; APPLICANT: Geysen, Hendrik M.
; TITLE OF INVENTION: Method for the use and synthesis of
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,213
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/752,437
; FILING DATE: 06-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO pct/au90/00062
; FILING DATE: 16-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P3788/89
; FILING DATE: 17-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
; REGISTRATION NUMBER: 31259
; REFERENCE/DOCKET NUMBER: 0240.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2706
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-475-213-10

Query Match 58.9%; Score 793; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 KEPLRPRCPINATLAVERKESCPVCITVNTTICAGYCPMTTRVLQGVLPALPOVVCNYRD 160
Db 2 KEPLRRCRPIINATLAVERKESCPVCITVNTTICAGYCPMTTRVLQGVLPALPOVVCNYRD 61
OY 161 VRESIRLPGCPRGVNVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFODSSSS 220
Db 62 VRESIRLPGCPRGVNVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFODSSSS 121
OY 221 KAPPSLSPSRRLGSPDTPILPOTS 244
Db 122 KAPPSLSPSRRLGSPDTPILPOTS 145

RESULT 6
US-08-395-238-2
; Sequence 2, Application US/08395238

Patent No. 5864488
GENERAL INFORMATION:
APPLICANT: ISSACS, Neil William
APPLICANT: LAPTHORN, Adrian Jonathan
APPLICANT: HARRIS, Deborah Claire
TITLE OF INVENTION: THREE DIMENSIONAL HORMONE STRUCTURE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: AKZO NOBEL PATENT DEPARTMENT
STREET: 1300 PICCARD DRIVE, SUITE 206
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: UNITED STATES
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,238
FILING DATE: 24-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9403600.1
FILING DATE: 24-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM M. BLACKSTONE
REGISTRATION NUMBER: 29,722
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BETA-SUBUNIT HUMAN CHORIONIC GONADOTROPIN
US-08-395-238-2

Query Match 58.9%: Score 793; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. NO. 1.7e-67;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRRCRPIINATLAVEKEGCPVITVNTTICAGYCPMTRVLOGVLPALPOVVCNRYD 160
DB 2 KEPLRRCRPIINATLAVEKEGCPVITVNTTICAGYCPMTRVLOGVLPALPOVVCNRYD 61

QY 161 VRFESIRLPGCGPRGVNPNVSYAVALSCCALCRSTTDCGPKDHPPLTCDDPRFODSSSS 220
DB 62 VRFESIRLPGCGPRGVNPNVSYAVALSCCALCRSTTDCGPKDHPPLTCDDPRFODSSSS 121

QY 221 KAPPSLPSPSRLPGPSDTPILPQ 244
DB 122 KAPPSLPSPSRLPGPSDTPILPQ 145

RESULT 7
US-09-142-320-12
Sequence 12, Application US/09142320
Patent No. 6194154
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique
APPLICANT: Bidart, Jean-Michel
APPLICANT: Vidaud, Michel
APPLICANT: Lazar, Vladimir
TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
FILE REFERENCE: 065691/0140
CURRENT APPLICATION NUMBER: US/09/142,320
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/FR97/00361

EARLIER FILING DATE: 1997-02-28
EARLIER APPLICATION NUMBER: FR 96 02683
EARLIER FILING DATE: 1996-03-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 12
LENGTH: 145
TYPE: PRT
ORGANISM: human
US-09-142-320-12

Query Match 58.9%: Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. NO. 1.7e-67;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRRCRPIINATLAVEKEGCPVITVNTTICAGYCPMTRVLOGVLPALPOVVCNRYD 160
DB 2 KEPLRRCRPIINATLAVEKEGCPVITVNTTICAGYCPMTRVLOGVLPALPOVVCNRYD 61

QY 161 VRFESIRLPGCGPRGVNPNVSYAVALSCCALCRSTTDCGPKDHPPLTCDDPRFODSSSS 220
DB 62 VRFESIRLPGCGPRGVNPNVSYAVALSCCALCRSTTDCGPKDHPPLTCDDPRFODSSSS 121

QY 221 KAPPSLPSPSRLPGPSDTPILPQ 244
DB 122 KAPPSLPSPSRLPGPSDTPILPQ 145

RESULT 8
US-09-142-320-13
Sequence 13, Application US/09142320
Patent No. 6194154
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique
APPLICANT: Bidart, Jean-Michel
APPLICANT: Vidaud, Michel
APPLICANT: Lazar, Vladimir
TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
FILE REFERENCE: 065691/0140
CURRENT APPLICATION NUMBER: US/09/142,320
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/FR97/00361
EARLIER FILING DATE: 1997-02-28
EARLIER APPLICATION NUMBER: FR 96 02683
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 13
LENGTH: 145
TYPE: PRT
ORGANISM: human
US-09-142-320-13

Query Match 58.9%: Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. NO. 1.7e-67;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRRCRPIINATLAVEKEGCPVITVNTTICAGYCPMTRVLOGVLPALPOVVCNRYD 160
DB 2 KEPLRRCRPIINATLAVEKEGCPVITVNTTICAGYCPMTRVLOGVLPALPOVVCNRYD 61

QY 161 VRFESIRLPGCGPRGVNPNVSYAVALSCCALCRSTTDCGPKDHPPLTCDDPRFODSSSS 220
DB 62 VRFESIRLPGCGPRGVNPNVSYAVALSCCALCRSTTDCGPKDHPPLTCDDPRFODSSSS 121

QY 221 KAPPSLPSPSRLPGPSDTPILPQ 244
DB 122 KAPPSLPSPSRLPGPSDTPILPQ 145

RESULT 9
US-09-142-320-14
Sequence 14, Application US/09142320

```

: Patent NO. 6194154
: GENERAL INFORMATION:
: APPLICANT: Bellet, Dominique
: APPLICANT: Bidart, Jean-Michel
: APPLICANT: Vidaud, Michel
: APPLICANT: Lazar, Vladimir
: TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION
: FILE REFERENCE: 065691/0140
: CURRENT APPLICATION NUMBER: US/09/142,320
: CURRENT FILING DATE: 1998-09-04
: EARLIER APPLICATION NUMBER: PCT/FR97/00361
: EARLIER FILING DATE: 1997-02-28
: EARLIER APPLICATION NUMBER: FR 96 02683
: EARLIER FILING DATE: 1996-03-04
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 145
: TYPE: PRT
: ORGANISM: human
: US-09-142-320-14

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Query Match	58.9%;	Score 793;	DB 4;	length 145;
Best Local Similarity	100.0%;	Pred. NO. 1.7e-67;		
Matches 144; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	101	KEPLRRCRPNATLAEKECCSPCIVNTTICAGYCPMTATRYLQGLPALPQVNCYRD	160
	2	KEPLRRCRPNATLAEKECCSPCIVNTTICAGYCPMTATRYLQGLPALPQVNCYRD	61
QY	161	VRESIRLPGCRPCVNVSVAVNLSCQALCRSTTDCGPKNRLTCDPPRODSSSS	220
Db	62	VRESIRLPGCRPCVNVSVAVNLSCQALCRSTTDCGPKNRLTCDPPRODSSSS	121
QY	221	KAPPSLPSRSRLGPPSDTPILPQ	244
	122	KAPPSLPSRSRLGPPSDTPILPQ	145
Db			

Db 122 KAPPSLPSPRLPGPDTPLPQ 145

```

RESULT 10
US-09-142-320-15
Sequence 15, Application US/09142320
Patent No. 6194154
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique
APPLICANT: Bidart, Jean-Michel
APPLICANT: Vidaud, Michel
APPLICANT: Lazart, Vladimir
TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION
DETECTION METHOD
FILE REFERENCE: 065691/0140
CURRENT APPLICATION NUMBER: US/09/142,320
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/FR97/00361
EARLIER FILING DATE: 1997-02-28
EARLIER APPLICATION NUMBER: FR 96 02683
EARLIER FILING DATE: 1996-03-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 145
TYPE: PRT
ORGANISM: human
US-09-142-320-15

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Query Match	58.9%	Score 793	DB 4	Length 145
Best Local Similarity	100.0%	Pred. No.	1.7e-67	
Matches 144; Conservative	0	Mismatches	0	Indels 0; Gaps 0;

[illegible]

Db	62	VRFESIRLPGCPRGVNPVSAVAALSCCALCRSTTDCGAPKHPILTCDDPRQDS	121
Oy	221	KAPPSLPSPSRLPGPSDTPILPQ	244
Db	122	KAPPSLPSPSRLPGPSDTPILPQ	145

RESULT 11
US-08-918-288-68
; Sequence 68, Application US/08918288
; Patent No. 6238890

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: STREET: 2000 Pennsylvania Avenue, NW, suite 5500
:
: CITY: Washington
:
: STATE: DC
:
: COUNTRY: USA
:
: ZIP: 20006-1888
:
: COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: diskette
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; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
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; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
;

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APPLICATION NUMBER: US/08/918,288
FILING DATE:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/282,357
; FILING DATE

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APPLCATION NUMBER: 08/853,524

; FILING DATE: 09-MAY-1997
 ; APPLICATION NUMBER: 08/199,382
 ;

FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H
REGISTRATION NUMBER: 38 050

REGISTRATION NUMBER: 25,555
REFERENCE/DOCKET NUMBER: 29500

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500

TELEFAX: 202-887-0763
TELETYPE:

INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids

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;      type: amino acid
;
;      STRANDEDNESS: single
;

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;          TOPOLOGY:  linear
HS-08-918-288-68

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Census Yearbook

E0 06

Census

Query match	38.9%;	Score
Best Local Similarity	100.0%;	Pre

Matches 144; Conservative 0; M

QY 101 KEPLRPRCPINATLAVEKEGCPVCITV

Db 2 KEPLRPRCRPINATLAVEKEGCPVCITV

QY 161 VRFESIRLPCCPRGVNPVSYAVALSCQ

Db 62 VFESIRLPGCCPGVNPVSYAVALSCC

0v 321 KAPBCT.BCBPI.BCBSTPI.BQ 3AA

221	KAE F O E I C F O N E F O I D D I F I D F Q	245
100		
	KAE F O E I C F O N E F O I D D I F I D F Q	

DB 122 KAPPSLEPSKLPGPSDIPLPQ 143

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RESULT 12
US-09-282-357-68
: Sequence 68 Application US/09282357
: Patent No. 6242580
: GENERAL INFORMATION:
: APPLICANT: BOIME, Irving
: APPLICANT: MOYLE, William R.
: TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
: TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTER
: NUMBER OF SEQUENCES: 83
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Avenue, NW, suite 5500
: City: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: Fastseq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/282,357
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/918,288
: FILING DATE: 25 AUG-1997
: APPLICATION NUMBER: 08/853,524
: FILING DATE: 09-MAY-1997
: APPLICATION NUMBER: 08/199,382
: FILING DATE: 18-FEB-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 29500-20050.25
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-887-1500
: TELEFAX: 202-887-0763
: TELEX:
: INFORMATION FOR SEQ ID NO: 68:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 145 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-282-357-68

Query Match 58.9%; Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 101 KELLPRRCRPINATLAVEEGCPVCTVNTTICAGYCPMTRVLQGVLPALQVVCNRYD 160
Db 2 KPELLPRRCRPINATLAVEEGCPVCTVNTTICAGYCPMTRVLQGVLPALQVVCNRYD 61
QY 161 VAFESIRLPGCRGVNPNVSVAVALSQCQALCRSTTDCGGRKDHPLTCDDEPRFODSSSS 220
Db 62 VAFESIRLPGCRGVNPNVSVAVALSQCQALCRSTTDCGGRKDHPLTCDDEPRFODSSSS 121
QY 221 KAPPSLPSPSRLPGSPDPILPQ 244
Db 122 KAPPSLPSPSRLPGSPDPILPQ 145

RESULT 13
US-08-908-371B-1
: Sequence 1, Application US/08908371B
: Patent No. 6331610
: GENERAL INFORMATION:
: APPLICANT: Bourinbalar, Aldar S.

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? TITLE OF INVENTION: A Method for Preventing and Treating
? TITLE OF INVENTION: AIDS and HIV Infection Using Select Peptides From the
? TITLE OF INVENTION: Beta Subunit of Human Chorionic Gonadotropin
? NUMBER OF SEQUENCES: 13
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Metatron, Inc.
? STREET: 367 Bay Shore Road
? CITY: Deer Park
? STATE: New York
? COUNTRY: United States of America
? ZIP: 11729
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 in. diskette (1.44megabytes)
? COMPUTER: IBM Compatible PC
? OPERATING SYSTEM: Windows 95
? SOFTWARE: WORD 6.0 ASCII TEXT CONVERSION ONLY
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/908,371B
? FILING DATE: 07-AUG-1997
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/044,937
? FILING DATE: 25-APR-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: COLEMAN, HENRY D.
? REGISTRATION NUMBER: 32,559
? REFERENCE/DOCKET NUMBER: M31-013
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 679-0090
? TELEFAX: (212) 679-9121
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 145 Amino Acid Units
? TYPE: Amino Acid
? STRANDEDNESS: Single Stranded
? TOPOLOGY: Linear
? MOLECULE TYPE: Protein Subunit
? DESCRIPTION: Amino Acid Corresponding to Beta Subunit
? DESCRIPTION: of Human Chorionic gonadotropin
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE: Sequence
? IMMEDIATE SOURCE: N/A
? POSITION IN GENOME: N/A
? FEATURE:
? NAME/KEY: 145 units of Beta Subunit of Human Chorionic
? NAME/KEY: Gonadotropin
? LOCATION: N/A
? IDENTIFICATION METHOD: Sequencing
? PUBLICATION INFORMATION:
? AUTHORS: CARLSEN, Robert B.,
? AUTHORS: BAHL, olm P.,
? AUTHORS: SWAMINATHAN, N.,
? TITLE: HUMAN CHORIONIC GONADOTROPIN
? JOURNAL: THE JOURNAL OF BIOLOGICAL CHEMISTRY
? VOLUME: 248
? PAGES: 6810-6825
? DATE: 1973
?
? US-08-908-371B-1
?
Query Match          58.9%; Score 793; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.7e-67;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      101 KEPLRPKRRPINALVAEKESGCPVITIVNTTICAGTCPTMTVLGGVLPALDPQVCNRYD    160
Db       2 KEPLRPKRRPINATLAVEKEGCPVICIVNTTICAGTCPTMTVLGGVLPALDPQVCNRYD    61
QY      161 VRFSIRILPGCGPRGVNVSVAAVALSCGALCRRTDDGCGPDHDLTCDDBRFDDSSSS    220
         |||||||
Db       62 VRFSIRILPGCGPRGVNVSVAAVALSCGALCRRTDDGCGPDHDLTCDDBRFDDSSSS    121
QY      221 KAPPSPLEPSRLPGPDSDTPIIPQ    244

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Db 122 KAPPSLPSPSRLLPGSPDPTLPQ 145

RESULT 14
US-08-709-924-2
; Sequence 2, Application US/08709924
; Patent No. 5968513
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
; TITLE OF INVENTION: USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,924
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-709-924-2

Query Match 58.6%; Score 790; DB 2; Length 165;
Best Local Similarity 99.3%; Pred. No. 3.9e-67;
Matches 143; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRPRCRPIMATLAVEKEGCPVCTIVNTTICAGYCPTMTRVLOGVLPALPOVVCNYRD 160
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Db 22 KEPLRPRCRPIMATLAVEKEGCPVCTIVNTTICAGYCPTMTRVLOGVLPALPOVVCNYRD 81
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QY 161 VRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFQDSSSS 220
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Db 82 VRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFQDSSSS 141

QY 221 KAPPSLPSPSRLLPGSPDPTLPQ 244
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Db 142 KAPPSLPSPSRLLPGSPDPTLPQ 165

RESULT 15
US-08-709-925-2
; Sequence 2, Application US/08709925
; Patent No. 5997871
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY

; TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROP
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,925
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 512
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-709-925-2

Query Match 58.6%; Score 790; DB 2; Length 165;
Best Local Similarity 99.3%; Pred. No. 3.9e-67;
Matches 143; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 101 KEPLRPRCRPIMATLAVEKEGCPVCTIVNTTICAGYCPTMTRVLOGVLPALPOVVCNYRD 160
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Db 22 KEPLRPRCRPIMATLAVEKEGCPVCTIVNTTICAGYCPTMTRVLOGVLPALPOVVCNYRD 81
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QY 161 VRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFQDSSSS 220
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Db 82 VRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDCGPKDHPILTCDDPRFQDSSSS 141

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Db 142 KAPPSLPSPSRLLPGSPDPTLPQ 165

Search completed: November 20, 2002, 17:29:32
Job time : 15.2727 secs

